of the present invention is directed to an isolated extracellular domain of a PRO733 polypeptide. Optionally, the PRO733 polypeptide is obtained or is obtainable by expressing the polypeptide encoded by the cDNA insert of the vector deposited on April 7, 1998 as DNA52196-1348.

71. PRO162

Applicants have identified a cDNA clone that encodes a novel polypeptide having sequence identity with pancreatitis-associated protein, wherein the polypeptide is designated in the present application as "PRO162".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO162 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO162 polypeptide having amino acid residues 1 through 175 of Figure 183 (SEQ ID NO:452), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. The isolated nucleic acid sequence may comprise the cDNA insert of the vector deposited on May 6, 1998 with the ATCC as DNA56965-1356 which includes the nucleotide sequence encoding PRO162.

In another embodiment, the invention provides isolated PRO162 polypeptide. In particular, the invention provides isolated native sequence PRO162 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 through 175 of Figure 183 (SEQ ID NO:452). Optionally, the PRO162 polypeptide is obtained or is obtainable by expressing the polypeptide encoded by the cDNA insert of the vector deposited on May 6, 1998 with the ATCC as DNA56965-1356.

72. PRO788

Applicants have identified a cDNA clone that encodes a novel polypeptide having sequence identity with anti-neoplastic urinary protein, wherein the polypeptide is designated in the present application as "PRO788".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO788 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO788 polypeptide having amino acid residues 1 through 125 of Figure 185 (SEQ ID NO:454), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. The isolated nucleic acid sequence may comprise the cDNA insert of the vector deposited on May 6, 1998 with the ATCC as DNA56405-1357 which includes the nucleotide sequence encoding PRO788.

In another embodiment, the invention provides isolated PRO788 polypeptide. In particular, the invention provides isolated native sequence PRO788 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 through 125 of Figure 185 (SEQ ID NO:454). An additional embodiment of the present invention is directed to an isolated extracellular domain of a PRO788 polypeptide. Optionally, the PRO788 polypeptide is obtained or is obtainable by expressing the polypeptide encoded by the cDNA insert of the vector deposited on May 6, 1998 with the ATCC as DNA56405-1357.

73. <u>PRO1008</u>

Applicants have identified a cDNA clone that encodes a novel polypeptide having sequence identity with dickkopf-1 (dkk-1), wherein the polypeptide is designated in the present application as "PRO1008".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO1008 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO1008 polypeptide having amino acid residues 1 through 266 of Figure 187 (SEQ ID NO:456), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. The isolated nucleic acid sequence may comprise the cDNA insert of the vector deposited on May 20, 1998 with the ATCC as DNA57530-1375 which includes the nucleotide sequence encoding PRO1008.

In another embodiment, the invention provides isolated PRO1008 polypeptide. In particular, the invention provides isolated native sequence PRO1008 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 through 266 of Figure 187 (SEQ ID NO:456). Optionally, the PRO1008 polypeptide is obtained or is obtainable by expressing the polypeptide encoded by the cDNA insert of the vector deposited on May 20, 1998 with the ATCC as DNA57530-1375.

In another embodiment, the invention provides an expressed sequence tag (EST) designated herein as DNA16508 comprising the nucleotide sequence of Figure 188 (SEQ ID NO:457).

74. <u>PRO1012</u>

Applicants have identified a cDNA clone that encodes a novel polypeptide having sequence identity with disulfide isomerase and phospholipase C, wherein the polypeptide is designated in the present application as "PRO1012".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO1012 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO1012 polypeptide having amino acid residues 1 through 747 of Figure 190 (SEQ ID NO:459), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. The isolated nucleic acid sequence may comprise the cDNA insert of the vector deposited on May 14, 1998 with the ATCC as DNA56439-1376, which includes the nucleotide sequence encoding PRO1012.

In another embodiment, the invention provides isolated PRO1012 polypeptide. In particular, the invention provides isolated native sequence PRO1012 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 through 747 of Figure 190 (SEQ ID NO:459). Optionally, the PRO1012 polypeptide is obtained or is obtainable by expressing the polypeptide encoded by the cDNA insert of the vector deposited on May 14, 1998 with the ATCC as DNA56439-1376.

75. **PRO1014**

Applicants have identified a cDNA clone that encodes a novel polypeptide having sequence identity with reductase, wherein the polypeptide is designated in the present application as "PRO1014".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO1014 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO1014 polypeptide having amino acid residues 1 through 300 of Figure 192 (SEQ ID NO:464), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. The isolated nucleic acid sequence may comprise the cDNA insert of the vector deposited on May 20, 1998 as DNA56409-1377 with the ATCC which includes the nucleotide sequence encoding PRO1014.

In another embodiment, the invention provides isolated PRO1014 polypeptide. In particular, the invention provides isolated native sequence PRO1014 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 through 300 of Figure 192 (SEQ ID NO:464). Optionally, the PRO1014 polypeptide is obtained or is obtainable by expressing the polypeptide encoded by the cDNA insert of the vector deposited on May 20, 1998 as DNA56409-1377 with the ATCC.

76. **PRO1017**

Applicants have identified a cDNA clone that encodes a novel polypeptide having sequence identity with HNK-1 sulfotransferase, wherein the polypeptide is designated in the present application as "PRO1017".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO1017 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO1017 polypeptide having amino acid residues 1 through 414 of Figure 194 (SEQ ID NO:466), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. The isolated nucleic acid sequence may comprise the cDNA insert of the vector deposited on May 20, 1998 with the ATCC as DNA56112-1379 which includes the nucleotide sequence encoding PRO1017.

In another embodiment, the invention provides isolated PRO1017 polypeptide. In particular, the invention provides isolated native sequence PRO1017 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 through 414 of Figure 194 (SEQ ID NO:466). Optionally, the PRO1017 polypeptide is obtained or is obtainable by expressing the polypeptide encoded by the cDNA insert of the vector deposited on May 20, 1998 with the ATCC as DNA56112-1379.

77. **PRO474**

Applicants have identified a cDNA clone that encodes a novel polypeptide having sequence identity with dehydrogenase, wherein the polypeptide is designated in the present application as "PRO474".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO474 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO474

polypeptide having amino acid residues 1 through 270 of Figure 196 (SEQ ID NO:468), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. The isolated nucleic acid sequence may comprise the cDNA insert of the vector deposited on May 14, 1998 with the ATCC as DNA56045-1380 which includes the nucleotide sequence encoding PRO474.

In another embodiment, the invention provides isolated PRO474 polypeptide. In particular, the invention provides isolated native sequence PRO474 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 through 270 of Figure 196 (SEQ ID NO:468). Optionally, the PRO474 polypeptide is obtained or is obtainable by expressing the polypeptide encoded by the cDNA insert of the vector deposited on May 14, 1998 with the ATCC as DNA56045-1380.

78. <u>PRO1031</u>

Applicants have identified a cDNA clone that encodes a novel polypeptide having sequence identity with IL-17, wherein the polypeptide is designated in the present application as "PRO1031".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO1031 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO1031 polypeptide having amino acid residues 1 through 180 of Figure 198 (SEQ ID NO:470), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. The isolated nucleic acid sequence may comprise the cDNA insert of the vector deposited on May 14, 1998 with the ATCC as DNA59294-1381 which includes the nucleotide sequence encoding PRO1031.

In another embodiment, the invention provides isolated PRO1031 polypeptide. In particular, the invention provides isolated native sequence PRO1031 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 through 180 of Figure 198 (SEQ ID NO:470). Optionally, the PRO1031 polypeptide is obtained or is obtainable by expressing the polypeptide encoded by the cDNA insert of the vector deposited on May 14, 1998 with the ATCC as DNA59294-1381.

79. <u>PRO938</u>

Applicants have identified a cDNA clone that encodes a novel polypeptide having sequence identity to protein disulfide isomerase, wherein the polypeptide is designated in the present application as "PRO938".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO938 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO938 polypeptide having amino acid residues 1 to 349 of Figure 200 (SEQ ID NO:472), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. In other aspects, the isolated nucleic acid comprises DNA encoding the PRO938 polypeptide having amino acid residues about 23 to 349 of Figure 200 (SEQ ID NO:472) or amino acid 1 or about 23 to X of Figure 200 (SEQ ID NO:472), where X is any amino acid from 186 to 195 of Figure 200 (SEQ

ID NO:472), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. The isolated nucleic acid sequence may comprise the cDNA insert of the DNA56433-1406 vector deposited on May 12, 1998, as ATCC Accession No. 209857 which includes the nucleotide sequence encoding PRO938.

In another embodiment, the invention provides isolated PRO938 polypeptide. In particular, the invention provides isolated native sequence PRO938 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 349 of Figure 200 (SEQ ID NO:472). Additional embodiments of the present invention are directed to PRO938 polypeptides comprising amino acids about 23 to 349 of Figure 200 (SEQ ID NO:472) or amino acid 1 or about 23 to X of Figure 200 (SEQ ID NO:472), where X is any amino acid from 186 to 195 of Figure 200 (SEQ ID NO:472). Optionally, the PRO938 polypeptide is obtained or is obtainable by expressing the polypeptide encoded by the cDNA insert of the DNA56433-1406 vector deposited on May 12, 1998, as ATCC Accession No. 209857.

80. PRO1082

Applicants have identified a cDNA clone that encodes a novel polypeptide having sequence identity with a lectin-like oxidized LDL receptor, wherein the polypeptide is designated in the present application as "PRO1082".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO1082 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO1082 polypeptide having amino acid residues 1 through 201 of Figure 202 (SEQ ID NO:477), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. The isolated nucleic acid sequence may comprise the cDNA insert of the vector deposited on May 14, 1998 with the ATCC as DNA53912-1457 which includes the nucleotide sequence encoding PRO1082.

In another embodiment, the invention provides isolated PRO1082 polypeptide. In particular, the invention provides isolated native sequence PRO1082 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 through 201 of Figure 202 (SEQ ID NO:477). An additional embodiment of the present invention is directed to an isolated domain of a PRO1082 polypeptide, excluding the transmembrane domain. Optionally, the PRO1082 polypeptide is obtained or is obtainable by expressing the polypeptide encoded by the cDNA insert of the vector deposited on May 14, 1998 with the ATCC as DNA53912-1457.

81. PRO1083

Applicants have identified a cDNA clone that encodes a novel polypeptide having sequence identity with a 7TM receptor, latrophilin-related protein 1, and a macrophage restricted cell surface glycoprotein, wherein the polypeptide is designated in the present application as "PRO1083".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding

a PRO1083 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO1083 polypeptide having amino acid residues 1 through 693 of Figure 204 (SEQ ID NO:483), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. The isolated nucleic acid sequence may comprise the cDNA insert of the vector deposited on May 12, 1998 with the ATCC as DNA50921-1458 which includes the nucleotide sequence encoding PRO1083.

In another embodiment, the invention provides isolated PRO1083 polypeptide. In particular, the invention provides isolated native sequence PRO1083 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 through 693 of Figure 204 (SEQ ID NO:483). An additional embodiment of the present invention is directed to an isolated extracellular domain of a PRO1083 polypeptide. Optionally, the PRO1083 polypeptide is obtained or is obtainable by expressing the polypeptide encoded by the cDNA insert of the vector deposited on May 12, 1998 with the ATCC as DNA50921-1458.

In another embodiment, the invention provides an expressed sequence tag (EST) designated herein as DNA24256 which comprises the nucleotide sequence of Figure 205 (SEQ ID NO:484).

82. <u>PRO200</u>

The objects of this invention, as defined generally <u>supra</u>, are achieved at least in part by the provision of a novel polypeptide, VEGF-E also herein designated PRO200, (SEQ ID NO:488) and the nucleic acid encoding therefor, SEQ ID NO:487, residues 259 through 1293.

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a VEGF-E polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the VEGF-E polypeptide having amino acid residues 1 through 345 of Figure 207 (SEQ ID NO:488), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under low stringency conditions. In another embodiment, variants are provided wherein the VEGF-E nucleic acid has single or multiple deletions, substitutions, insertions, truncations or combinations thereof.

In another embodiment, the invention provides isolated VEGF-E polypeptide. In particular, the invention provides an isolated native sequence VEGF-E polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 through 345 of Figure 207 (SEQ ID NO:488). In another embodiment, variants are provided wherein the VEGF-E polypeptide has single or multiple deletions, substitutions, insertions, truncations or combinations thereof.

In yet further embodiments, the present invention is directed to compositions useful for treating indications where proliferation, survival and/or differentiation of cells is desired, comprising a therapeutically effective amount of a VEGF-E polypeptide hereof in admixture with a pharmaceutically acceptable carrier.

The invention further includes associated embodiments of VEGF-E such as modified VEGF-E polypeptides and modified variants which have the same biological applications as VEGF-E, and pharmaceutical compositions incorporating same. Inhibitors of VEGF-E are also provided.

83. **PRO285 and PRO286**

Applicants have identified two novel cDNA clones that encode novel human Toll polypeptides, designated in the present application as PRO285 (encoded by DNA40021-1154) and PRO286 (encoded by DNA42663-1154).

In one embodiment, the invention provides an isolated nucleic acid molecule comprising a DNA encoding a polypeptide having at least about 80% sequence identity, preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, most preferably at least about 95% sequence identity to (a) a DNA molecule encoding a PRO285 polypeptide having amino acid residues 27 to 839 of Figure 209 (SEQ ID NO:496); or (b) to a DNA molecule encoding a PRO286 polypeptide having amino acid residues 27 to 825 of Figure 211 (SEQ ID NO:498) or (c) the complement of the DNA molecule of (a) or (b). The complementary DNA molecule preferably remains stably bound to such encoding nucleic acid sequence under at least moderate, and optionally, under high stringency conditions.

In a further embodiment, the isolated nucleic acid molecule comprises a polynucleotide that has at least about 90%, preferably at least about 95% sequence identity with a polynucleotide encoding a polypeptide comprising the sequence of amino acids 1 to 839 of Figure 209 (SEQ ID NO:496); or at least about 90%, preferably at least about 95% sequence identity with a polynucleotide encoding a polypeptide comprising the sequence of amino acids 1 to 1041 of Figure 211 (SEQ ID NO:498).

In a specific embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding native or variant PRO285 and PRO286 polypeptides, with or without the N-terminal signal sequence, and with or without the transmembrane regions of the respective full-length sequences. In one aspect, the isolated nucleic acid comprises DNA encoding a mature, full-length native PRO285 or PRO286 polypeptide having amino acid residues 1 to 1049 of Figure 209 (SEQ ID NO:496) and 1 to 1041 of Figure 211 (SEQ ID NO: 498), or is complementary to such encoding nucleic acid sequence. In another aspect, the invention concerns an isolated nucleic acid molecule that comprises DNA encoding a native PRO285 or PRO286 polypeptide without an N-terminal signal sequence, or is complementary to such encoding nucleic acid sequence. In yet another embodiment, the invention concerns nucleic acid encoding transmembrane-domain deleted or inactivated forms of the full-length native PRO285 or PRO286 proteins.

In another embodiment, the invention the isolated nucleic acid molecule comprises the clone (DNA40021-1154) deposited on October 17, 1997, under ATCC number 209389; or the clone (DNA42663-1154) deposited on October 17, 1997, under ATCC number 209386.

In yet another embodiment, the invention provides a vector comprising DNA encoding PRO285 and PRO286 polypeptides, or their variants. Thus, the vector may comprise any of the isolated nucleic acid molecules hereinabove defined.

In another embodiment, the invention provides isolated PRO285 and PRO286 polypeptides. In particular, the invention provides isolated native sequence PRO285 and PRO286 polypeptides, which in one embodiment, include the amino acid sequences comprising residues 1 to 1049 and 1 to 1041 of Figures 209 and 211 (SEQ ID NOS:496 and 498), respectively. The invention also provides for variants of the PRO285 and

PRO286 polypeptides which are encoded by any of the isolated nucleic acid molecules hereinabove defined. Specific variants include, but are not limited to, deletion (truncated) variants of the full-length native sequence PRO285 and PRO286 polypeptides which lack the respective N-terminal signal sequences and/or have their respective transmembrane and/or cytoplasmic domains deleted or inactivated.

The invention also specifically includes antibodies with dual specificities, e.g., bispecific antibodies binding more than one Toll polypeptide.

In yet another embodiment, the invention concerns agonists and antagonists of the native PRO285 and PRO286 polypeptides. In a particular embodiment, the agonist or antagonist is an anti-PRO285 or anti-PRO286 antibody.

In a further embodiment, the invention concerns screening assays to identify agonists or antagonists of the native PRO285 and PRO286 polypeptides.

In a still further embodiment, the invention concerns a composition comprising a PRO285 or PRO286 polypeptide, or an agonist or antagonist as hereinabove defined, in combination with a pharmaceutically acceptable carrier.

The invention further concerns a composition comprising an antibody specifically binding a PRO285 or PRO286 polypeptide, in combination with a pharmaceutically acceptable carrier.

The invention also concerns a method of treating septic shock comprising administering to a patient an effective amount of an antagonist of a PRO285 or PRO286 polypeptide. In a specific embodiment, the antagonist is a blocking antibody specifically binding a native PRO285 or PRO286 polypeptide.

84. PRO213-1, PRO1330 and PRO1449

The present invention concerns compositions and methods for the diagnosis and treatment of neoplastic cell growth and proliferation in mammals, including humans. The present invention is based on the identification of genes that are amplified in the genome of tumor cells. Such gene amplification is expected to be associated with the overexpression of the gene product and contribute to tumorigenesis. Accordingly, the proteins encoded by the amplified genes are believed to be useful targets for the diagnosis and/or treatment (including prevention) of certain cancers, and may act as predictors of the prognosis of tumor treatment.

In one embodiment, the present invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO213-1, PRO1330 and/or PRO1449 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO213-1, PRO1330 and/or PRO1449 polypeptide having amino acid residues 1 to 295 of Figure 213 (SEQ ID NO:506), 20 to 273 of Figure 215 (SEQ ID NO:508) and 20 to 273 of Figure 217 (SEQ ID NO:510), respectively, or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. The isolated nucleic acid sequence may comprise the cDNA insert of the vector designated as DNA30943-1163 (ATCC 209791) deposited on April 21, 1998; DNA64907-1163-1 (ATCC 203242) deposited on September 9, 1998 and/or DNA64908-1163-1 (ATCC 203243) deposited on September 9, 1998.

In another embodiment, the present invention comprises an isolated nucleic acid molecule having at least

about 80% sequence identity, preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, most preferably at least about 95% sequence identity to (a) a DNA molecule encoding a PRO213-1, PRO1330 and/or PRO1449 polypeptide having amino acid residues 1 to 295 of Figure 213 (SEQ ID NO:506), 20 to 273 of Figure 215 (SEQ ID NO:508) and 20 to 273 of Figure 217 (SEQ ID NO:510), respectively; or (b) the complement of the DNA molecule of (a).

In another embodiment, the invention provides an isolated PRO213-1, PRO1330 and/or PRO1449 polypeptide. In particular, the invention provides isolated native sequence PRO213-1, PRO1330 and/or PRO1449 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 295 of Figure 213 (SEQ ID NO:506), 20 to 273 of Figure 215 (SEQ ID NO:508) or 20 to 273 of Figure 217 (SEQ ID NO:510), respectively. Optionally, the PRO213-1, PRO1330 and/or PRO1449 polypeptide is obtained or obtainable by expressing the polypeptide encoded by the cDNA insert of the DNA30943-1163 (ATCC 209791), DNA64907-1163-1 (ATCC 203242) or DNA64908-1163-1 (ATCC 203243).

In another aspect, the invention provides an isolated PRO213-1, PRO1330, and/or PRO1449 polypeptide, comprising an amino acid sequence having at least about 80% sequence identity, preferably at least about 85% sequence identity, more preferably at least about 95% sequence identity to amino acid residues 1 to 295 of Figure 213 (SEQ ID NO:506), 20 to 273 of Figure 215 (SEQ ID NO:508) or 20 to 273 of Figure 217 (SEQ ID NO:510), inclusive.

In yet another embodiment, the invention provides an isolated PRO213-1, PRO1330, and/or PRO1449 polypeptide, comprising the amino acid residues 1 to 295 of Figure 213 (SEQ ID NO:506), 20 to 273 of Figure 215 (SEQ ID NO:508) or 20 to 273 of Figure 217 (SEQ ID NO:510), or a fragment thereof sufficient to provide a binding site for an anti-PRO213-1, anti-PRO1330 and/or anti-PRO1449 antibody. Preferably, the PRO213-1, PRO1330, and/or PRO1449 fragment retains a qualitative biological activity of a native PRO213-1, PRO1330, and/or PRO1449 polypeptide.

In a further aspect, the invention concerns an isolated PRO213-1, PRO1330, and/or PRO1449 polypeptide, comprising an amino acid sequence scoring at least about 80% positives, preferably at least about 85% positives, more preferably at least about 90% positives, most preferably at least about 95% positives when compared with the amino acid sequence of residues 1 to 295 of Figure 213 (SEQ ID NO:506), 20 to 273 of Figure 215 (SEQ ID NO:508) and 20 to 273 of Figure 217 (SEQ ID NO:510), respectively.

In still a further aspect, the invention provides a polypeptide produced by (i) hybridizing a test DNA molecule under stringent conditions with: (a) a DNA molecule encoding a PRO213-1, PRO1330, and/or PRO1449 polypeptide having the amino acid residues from 1 to 295 of Figure 213 (SEQ ID NO:506), 20 to 273 of Figure 215 (SEQ ID NO:508) and 20 to 273 of Figure 217 (SEQ ID NO:510), respectively; or the complement of the DNA molecule of (a), and if said test DNA molecule has at least about an 80% sequence identity to (a) or (b), (ii) culturing a host cell comprising said test DNA molecule under conditions suitable for the expression of said polypeptide, and (iii) recovering said polypeptide from the cell culture.

In one embodiment, the present invention concerns an isolated antibody which binds a PRO213-1, PRO1330 and/or PRO1449 polypeptide. In one aspect, the antibody induces death of a cell overexpressing a

PRO213-1, PRO1330 and/or PRO1449 polypeptide. In another aspect, the antibody is a monoclonal antibody, which preferably has nonhuman complementarity determining region (CDR) residues and human framework region (FR) residues. The antibody may be labeled and may be immobilized on a solid support. In a further aspect, the antibody is an antibody fragment, a single-chain antibody, or an anti-idiotypic antibody.

In another embodiment, the invention concerns a composition comprising an antibody which binds a PRO213-1, PRO1330 and/or PRO1449 polypeptide in admixture with a pharmaceutically acceptable carrier. In one aspect, the composition comprises a therapeutically effective amount of the antibody. In another aspect, the composition comprises a further active ingredient, which may, for example, be a further antibody or a cytotoxic or chemotherapeutic agent. Preferably, the composition is sterile.

In a further embodiment, the invention concerns nucleic acid encoding an anti-PRO213-1, anti-PRO1330 and/or anti-PRO1449 antibody, and vectors and recombinant host cells comprising such nucleic acid.

The invention further concerns antagonists and agonists of a PRO213-1, PRO1330 and/or PRO1449 polypeptide that inhibit one or more of the functions or activities of the PRO213-1, PRO1330 and/or PRO1449 polypeptide.

In a further embodiment, the invention concerns isolated nucleic acid molecules that hybridize to the complement of the nucleic acid molecules encoding the PRO213-1, PRO1330 and/or PRO1449 polypeptides. The nucleic acid preferably is DNA, and hybridization preferably occurs under stringent conditions. Such nucleic acid molecules can act as antisense molecules of the amplified genes identified herein, which, in turn, can find use in the modulation of the respective amplified genes, or as antisense primers in amplification reactions. Furthermore, such sequences can be used as part of ribozyme and/or triple helix sequence which, in turn, may be used in regulation of the amplified genes.

In another embodiment, the invention concerns a method for determining the presence of a PRO213-1, PRO1330 and/or PRO1449 polypeptide comprising exposing a cell suspected of containing the PRO213-1, PRO1330 and/or PRO1449 polypeptide to an anti-PRO213-1, PRO1330 and/or PRO1449 antibody and determining binding of the antibody to the cell.

In yet another embodiment, the present invention concerns a method of diagnosing tumor in a mammal, comprising detecting the level of expression of a gene encoding a PRO213-1, PRO1330 and/or PRO1449 polypeptide (a) in a test sample of tissue cells obtained from the mammal, and (b) in a control sample of known normal tissue cells of the same cell type, wherein a higher expression level in the test sample indicates the presence of tumor in the mammal from which the test tissue cells were obtained.

In another embodiment, the present invention concerns a method of diagnosing tumor in a mammal, comprising (a) contacting an anti-PRO213-1, anti-PRO1330 and/or anti-PRO1449 antibody with a test sample of tissue cells obtained from the mammal, and (b) detecting the formation of a complex between the anti-PRO213-1, anti-PRO1330 and/or anti-PRO1449 antibody and the PRO213-1, PRO1330 and/or PRO1449 polypeptide in the test sample. The detection may be qualitative or quantitative, and may be performed in comparison with monitoring the complex formation in a control sample of known normal tissue cells of the same cell type. A larger quantity of complexes formed in the test sample indicates the presence of tumor in the

mammal from which the test tissue cells were obtained. The antibody preferably carries a detectable label. Complex formation can be monitored, for example, by light microscopy, flow cytometry, fluorimetry, or other techniques known in the art. The test sample is usually obtained from an individual suspected to have neoplastic cell growth or proliferation (e.g. cancerous cells).

In another embodiment, the present invention concerns a cancer diagnostic kit, comprising an anti-PRO213-1, anti-PRO1330 and/or anti-PRO1449 antibody and a carrier (e.g. a buffer) in suitable packaging. The kit preferably contains instructions for using the antibody to detect the PRO213-1, PRO1330 and/or PRO1449 polypeptide.

In yet another embodiment, the invention concerns a method for inhibiting the growth of tumor cells comprising exposing a cell which overexpresses a PRO213-1, PRO1330 and/or PRO1449 polypeptide to an effective amount of an agent inhibiting the expression and/or activity of the PRO213-1, PRO1330 and/or PRO1449 polypeptide. The agent preferably is an anti-PRO213-1, anti-PRO1330 and/or anti-PRO1449 antibody, a small organic and inorganic molecule, peptide, phosphopeptide, antisense or ribozyme molecule, or a triple helix molecule. In a specific aspect, the agent, e.g. anti-PRO213-1, anti-PRO1330 and/or anti-PRO1449 antibody induces cell death. In a further aspect, the tumor cells are further exposed to radiation treatment and/or a cytotoxic or chemotherapeutic agent.

In a further embodiment, the invention concerns an article of manufacture, comprising:

a) a container;

b) a label on the container; and

c) a composition comprising an active agent contained within the container; wherein the composition is effective for inhibiting the growth of tumor cells, the label on the container indicates that the composition can be used for treating conditions characterized by overexpression of a PRO213-1, PRO1330 and/or PRO1449 polypeptide, and the active agent in the composition is an agent inhibiting the expression and/or activity of the PRO213-1, PRO1330 and/or PRO1449 polypeptide. In a preferred aspect, the active agent is an anti-PRO213-1, anti-PRO1330 and/or anti-PRO1449 antibody.

In yet a further embodiment, the invention provides a method for identifying a compound capable of inhibiting the expression and/or activity of a PRO213-1, PRO1330 and/or PRO1449 polypeptide, comprising contacting a candidate compound with a PRO213-1, PRO1330 and/or PRO1449 polypeptide under conditions and for a time sufficient to allow these two components to interact. In a specific aspect, either the candidate compound or the PRO213-1, PRO1330 and/or PRO1449 polypeptide is immobilized on a solid support. In another aspect, the non-immobilized component carries a detectable label.

85. PRO298

Applicants have identified a cDNA clone that encodes a novel polypeptide. The DNA is designated in the present application as "DNA39975-1210", encoding a novel multi-transmembrane protein, referred to as "PRO298".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA having

at least about 80%, preferably at least about 85%, more preferably at least about 90%, most preferably at least about 95% sequence identity to (a) a DNA molecule encoding PRO298, comprising the sequence of amino acids 1 to 364 of Figure 219 (SEQ ID NO:515), or (b) the complement of the DNA molecule of (a). In one aspect, the isolated nucleic acid comprises DNA encoding a PRO298 polypeptide having amino acid residues 1 to 364 of Figure 219 (SEQ ID NO:515), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In a further embodiment, the invention concerns an isolated nucleic acid molecule comprising DNA having at least an 80% sequence identity to (a) a DNA molecule encoding the same mature polypeptide encoded by the human protein cDNA in ATCC Deposit No. 209783 (DNA39975-1210), or (b) the complement of the DNA molecule of (a).

In a still further embodiment, the invention concerns nucleic acid which comprises a DNA molecule encoding the same mature polypeptide encoded by the human protein cDNA in ATCC Deposit No. 209783 (DNA39975-1210).

In another embodiment, the invention provides isolated PRO298 polypeptide. In particular, the invention provides isolated native sequence PRO298 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 364 of Figure 219 (SEQ ID NO:515).

In another embodiment, the invention provides an expressed sequence tag (EST) designated DNA26832 comprising the nucleotide sequence of Figure 220 (SEQ ID NO:516).

86. PRO337

Applicants have identified a cDNA clone (DNA43316-1237) that encodes a novel polypeptide, designated in the present application as "PRO337".

In one embodiment, the invention provides an isolated nucleic acid molecule having at least about 80% sequence identity to (a) a DNA molecule encoding a PRO337 polypeptide comprising the sequence of amino acids 1 to 344 of Figure 222 (SEQ ID NO:523), or (b) the complement of the DNA molecule of (a). The sequence identity preferably is about 85%, more preferably about 90%, most preferably about 95%. In one aspect, the isolated nucleic acid has at least about 80%, preferably at least about 85%, more preferably at least about 90%, and most preferably at least about 95 (including 96, 97, 98 and 99%) sequence identity with a polypeptide having amino acid residues 1 to 344 of Figure 222 (SEQ ID NO:523). Preferably, the highest degree of sequence identity occurs within the immunoglobulin and major histocompatibility domains (amino acids 113 to 130 of Figure 222, SEQ ID NO:523).

In a further embodiment, the isolated nucleic acid molecule comprises DNA encoding a neurotrimin polypeptide having amino acid residues 1 to 344 of Figure 222 (SEQ ID NO:523), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. In another aspect, the invention provides a nucleic acid of the full length protein of clone DNA43316-1237, deposited with the ATCC under accession number ATCC 209487, alternatively the coding sequence of clone DNA43316-1237, deposited under accession number ATCC 209487.

In yet another embodiment, the invention provides isolated PRO337 polypeptide. In particular, the invention provides isolated native sequence PRO337 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 344 of Figure 222 (SEQ ID NO:523). Native PRO337 polypeptides with or without the native signal sequence (amino acids 1 to about 28 in Figure 222 (SEQ ID NO:523), and with or without the initiating methionine are specifically included. Alternatively, the invention provides a PRO337 polypeptide encoded by the nucleic acid deposited under accession number ATCC 209487.

In yet another embodiment, the invention provides an expressed sequence tag (EST) comprising the nucleotide sequences identified in Figure 223 as DNA42301 (SEQ ID NO:524).

87. PRO403

Applicants have identified a cDNA clone (DNA55800-1263) that encodes a novel polypeptide, designated in the present application as "PRO403".

In one embodiment, the invention provides an isolated nucleic acid molecule having at least about 80% sequence identity to (a) a DNA molecule encoding a PRO403 polypeptide comprising the sequence of amino acids 1 to 736 of Figure 225 (SEQ ID NO:526), or (b) the complement of the DNA molecule of (a). The sequence identity preferably is about 85%, more preferably about 90%, most preferably about 95%. In one aspect, the isolated nucleic acid has at least about 80%, preferably at least about 85%, more preferably at least about 90%, and most preferably at least about 95% sequence identity with a polypeptide having amino acid residues 1 to 736 of Figure 225 (SEQ ID NO:526). Preferably, the highest degree of sequence identity occurs within: (1) the putative N-glycosylatation sites (amino acid residues 132, 136, 177, 237, 282, 349, 505, 598 and 606; (2) Cys residues conserved with the Kell blood group protein family (amino acid residues 65, 70, 88 and 96) and the putative zinc binding motif (amino acid residues 570-579).

In a further embodiment, the isolated nucleic acid molecule comprises DNA encoding a PRO403 polypeptide having amino acid residues 1 to 736 of Figure 225 (SEQ ID NO:526), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. In another aspect, the invention provides a nucleic acid of the full length protein of clone DNA55800-1263, deposited with the ATCC under accession number ATCC 209680, alternatively the coding sequence of clone DNA55800-1263, deposited under accession number ATCC 209680.

In yet another embodiment, the invention provides isolated PRO403 polypeptide. In particular, the invention provides isolated native sequence PRO403 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 736 of Figure 225 (SEQ ID NO:526). Native PRO403 polypeptides with or the initiating methionine are specifically included. Alternatively, the invention provides a PRO403 polypeptide encoded by the nucleic acid deposited under accession number ATCC 209680.

In yet another embodiment, the invention provides an expressed sequence tag (EST) and other sequence fragments comprising the nucleotide sequences identified herein as DNA34415 (Figures 226A-B; SEQ ID NO:527); DNA49830 (Figure 227 ; SEQ ID NO:528) and DNA49831 (Figure 228; SEQ ID NO:529).

88. **Additional Embodiments**

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the above or below described polypeptides. A host cell comprising any such vector is also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the above or below described polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

In other embodiments, the invention provides chimeric molecules comprising any of the above or below described polypeptides fused to a heterologous polypeptide or amino acid sequence. An example of such a chimeric molecule comprises any of the above or below described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which specifically binds to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody.

In yet other embodiments, the invention provides oligonucleotide probes useful for isolating genomic and cDNA nucleotide sequences, wherein those probes may be derived from any of the above or below described nucleotide sequences.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO213 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "UNQ187" and/or "DNA30943-1163".

Figure 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in Figure 1.

Figure 3 shows a nucleotide sequence (SEQ ID NO:6) of a native sequence PRO274 cDNA, wherein SEQ ID NO:6 is a clone designated herein as "UNQ241" and/or "DNA39987-1184".

Figure 4 shows the amino acid sequence (SEQ ID NO:7) derived from the coding sequence of SEQ ID NO:6 shown in Figure 3.

Figure 5 shows an EST nucleotide sequence designated herein as DNA17873 (SEQ ID NO:8).

Figure 6 shows an EST nucleotide sequence designated herein as DNA36157 (SEQ ID NO:9).

Figure 7 shows an EST nucleotide sequence designated herein as DNA28929 (SEQ ID NO:10).

Figure 8 shows a nucleotide sequence (SEQ ID NO:18) of a native sequence PRO300 cDNA, wherein SEQ ID NO:18 is a clone designated herein as "UNQ263" and/or "DNA40625-1189".

Figure 9 shows the amino acid sequence (SEQ ID NO:19) derived from the coding sequence of SEQ ID NO:18 shown in Figure 8.

Figure 10 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO284 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "UNQ247" and/or "DNA23318-1211".

Figure 11 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in Figure 10.

Figure 12 shows an EST nucleotide sequence designated herein as DNA12982 (SEQ ID NO:29).

Figure 13 shows an EST nucleotide sequence designated herein as DNA15886 (SEQ ID NO:30).

Figure 14 shows a nucleotide sequence (SEQ ID NO:35) of a native sequence PRO296 cDNA, wherein SEQ ID NO:35 is a clone designated herein as "UNQ260" and/or "DNA39979-1213".

Figure 15 shows the amino acid sequence (SEQ ID NO:36) derived from the coding sequence of SEQ ID NO:35 shown in Figure 14.

Figure 16 shows an EST nucleotide sequence designated herein as DNA23020 (SEQ ID NO:37).

Figure 17 shows an EST nucleotide sequence designated herein as DNA21971 (SEQ ID NO:38).

Figure 18 shows an EST nucleotide sequence designated herein as DNA29037 (SEQ ID NO:39).

Figure 19 shows a nucleotide sequence (SEQ ID NO:44) of a native sequence PRO329 cDNA, wherein SEQ ID NO:44 is a clone designated herein as "UNQ291" and/or "DNA40594-1233".

Figure 20 shows the amino acid sequence (SEQ ID NO:45) derived from the coding sequence of SEQ ID NO:44 shown in Figure 19.

Figure 21 shows a nucleotide sequence (SEQ ID NO:51) of a native sequence PRO362 cDNA, wherein SEQ ID NO:51 is a clone designated herein as "UNQ317" and/or "DNA45416-1251".

Figure 22 shows the amino acid sequence (SEQ ID NO:52) derived from the coding sequence of SEQ ID NO:51 shown in Figure 21.

Figure 23 shows a nucleotide sequence (SEQ ID NO:58) of a native sequence PRO363 cDNA, wherein SEQ ID NO:58 is a clone designated herein as "UNQ318" and/or "DNA45419-1252".

Figure 24 shows the amino acid sequence (SEQ ID NO:59) derived from the coding sequence of SEQ ID NO:58 shown in Figure 23.

Figure 25 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO868 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "UNQ437" and/or "DNA52594-1270".

Figure 26 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in Figure 25.

Figure 27 shows a nucleotide sequence (SEQ ID NO:68) of a native sequence PRO382 cDNA, wherein SEQ ID NO:68 is a clone designated herein as "UNQ323" and/or "DNA45234-1277".

Figure 28 shows the amino acid sequence (SEQ ID NO:69) derived from the coding sequence of SEQ ID NO:68 shown in Figure 27.

Figure 29 shows a nucleotide sequence (SEQ ID NO:73) of a native sequence PRO545 cDNA, wherein SEQ ID NO:73 is a clone designated herein as "UNQ346" and/or "DNA49624-1279".

Figure 30 shows the amino acid sequence (SEQ ID NO:74) derived from the coding sequence of SEQ ID NO:73 shown in Figure 29.

Figure 31 shows an EST nucleotide sequence designated herein as DNA13217 (SEQ ID NO:75).

Figure 32 shows a nucleotide sequence (SEQ ID NO:84) of a native sequence PRO617 cDNA, wherein SEQ ID NO:84 is a clone designated herein as "UNQ353" and/or "DNA48309-1280".

Figure 33 shows the amino acid sequence (SEQ ID NO:85) derived from the coding sequence of SEQ

ID NO:84 shown in Figure 32.

Figure 34 shows a nucleotide sequence (SEQ ID NO:89) of a native sequence PRO700 cDNA, wherein SEQ ID NO:89 is a clone designated herein as "UNQ364" and/or "DNA46776-1284".

Figure 35 shows the amino acid sequence (SEQ ID NO:90) derived from the coding sequence of SEQ ID NO:89 shown in Figure 34.

Figure 36 shows a nucleotide sequence (SEQ ID NO:96) of a native sequence PRO702 cDNA, wherein SEQ ID NO:96 is a clone designated herein as "UNQ366" and/or "DNA50980-1286".

Figure 37 shows the amino acid sequence (SEQ ID NO:97) derived from the coding sequence of SEQ ID NO:96 shown in Figure 36.

Figure 38 shows a nucleotide sequence (SEQ ID NO:101) of a native sequence PRO703 cDNA, wherein SEQ ID NO:101 is a clone designated herein as "UNQ367" and/or "DNA50913-1287".

Figure 39 shows the amino acid sequence (SEQ ID NO:102) derived from the coding sequence of SEQ ID NO:101 shown in Figure 38.

Figure 40 shows a nucleotide sequence (SEQ ID NO:108) of a native sequence PRO705 cDNA, wherein SEQ ID NO:108 is a clone designated herein as "UNQ369" and/or "DNA50914-1289".

Figure 41 shows the amino acid sequence (SEQ ID NO:109) derived from the coding sequence of SEQ ID NO:108 shown in Figure 40.

Figures 42A-B show a nucleotide sequence (SEQ ID NO:113) of a native sequence PRO708 cDNA, wherein SEQ ID NO:113 is a clone designated herein as "UNQ372" and/or "DNA48296-1292".

Figure 43 shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113 shown in Figures 42A-B.

Figure 44 shows a nucleotide sequence (SEQ ID NO:118) of a native sequence PRO320 cDNA, wherein SEQ ID NO:118 is a clone designated herein as "UNQ281" and/or "DNA32284-1307".

Figure 45 shows the amino acid sequence (SEQ ID NO:119) derived from the coding sequence of SEQ ID NO:118 shown in Figure 44.

Figure 46 shows a nucleotide sequence (SEQ ID NO:123) of a native sequence PRO324 cDNA, wherein SEQ ID NO:123 is a clone designated herein as "UNQ285" and/or "DNA36343-1310".

Figure 47 shows the amino acid sequence (SEQ ID NO:124) derived from the coding sequence of SEQ ID NO:123 shown in Figure 46.

Figure 48 shows a nucleotide sequence (SEQ ID NO:131) of a native sequence PRO351 cDNA, wherein SEQ ID NO:131 is a clone designated herein as "UNQ308" and/or "DNA40571-1315".

Figure 49 shows the amino acid sequence (SEQ ID NO:132) derived from the coding sequence of SEQ ID NO:131 shown in Figure 48.

Figure 50 shows a nucleotide sequence (SEQ ID NO:136) of a native sequence PRO352 cDNA, wherein SEQ ID NO:136 is a clone designated herein as "UNQ309" and/or "DNA41386-1316".

Figure 51 shows the amino acid sequence (SEQ ID NO:137) derived from the coding sequence of SEQ ID NO:136 shown in Figure 50.

Figure 52 shows a nucleotide sequence (SEQ ID NO:144) of a native sequence PRO381 cDNA, wherein SEQ ID NO:144 is a clone designated herein as "UNQ322" and/or "DNA44194-1317".

Figure 53 shows the amino acid sequence (SEQ ID NO:145) derived from the coding sequence of SEQ ID NO:144 shown in Figure 52.

Figure 54 shows a nucleotide sequence (SEQ ID NO:149) of a native sequence PRO386 cDNA, wherein SEQ ID NO:149 is a clone designated herein as "UNQ326" and/or "DNA45415-1318".

Figure 55 shows the amino acid sequence (SEQ ID NO:150) derived from the coding sequence of SEQ ID NO:149 shown in Figure 54.

Figure 56 shows an EST nucleotide sequence designated herein as DNA23350 (SEQ ID NO:151).

Figure 57 shows an EST nucleotide sequence designated herein as DNA23536 (SEQ ID NO:152).

Figure 58 shows a nucleotide sequence (SEQ ID NO:156) of a native sequence PRO540 cDNA, wherein SEQ ID NO:156 is a clone designated herein as "UNQ341" and/or "DNA44189-1322".

Figure 59 shows the amino acid sequence (SEQ ID NO:157) derived from the coding sequence of SEQ ID NO:156 shown in Figure 58.

Figure 60 shows a nucleotide sequence (SEQ ID NO:161) of a native sequence PRO615 cDNA, wherein SEQ ID NO:161 is a clone designated herein as "UNQ352" and/or "DNA48304-1323".

Figure 61 shows the amino acid sequence (SEQ ID NO:162) derived from the coding sequence of SEQ ID NO:161 shown in Figure 60.

Figure 62 shows a nucleotide sequence (SEQ ID NO:168) of a native sequence PRO618 cDNA, wherein SEQ ID NO:168 is a clone designated herein as "UNQ354" and/or "DNA49152-1324".

Figure 63 shows the amino acid sequence (SEQ ID NO:169) derived from the coding sequence of SEQ ID NO:168 shown in Figure 62.

Figure 64 shows an EST nucleotide sequence designated herein as DNA35597 (SEQ ID NO:170).

Figure 65 shows a nucleotide sequence (SEQ ID NO:177) of a native sequence PRO719 cDNA, wherein SEQ ID NO:177 is a clone designated herein as "UNQ387" and/or "DNA49646-1327".

Figure 66 shows the amino acid sequence (SEQ ID NO:178) derived from the coding sequence of SEQ ID NO:177 shown in Figure 65.

Figure 67 shows a nucleotide sequence (SEQ ID NO:182) of a native sequence PRO724 cDNA, wherein SEQ ID NO:182 is a clone designated herein as "UNQ389" and/or "DNA49631-1328".

Figure 68 shows the amino acid sequence (SEQ ID NO:183) derived from the coding sequence of SEQ ID NO:182 shown in Figure 67.

Figure 69 shows a nucleotide sequence (SEQ ID NO:189) of a native sequence PRO772 cDNA, wherein SEQ ID NO:189 is a clone designated herein as "UNQ410" and/or "DNA49645-1347".

Figure 70 shows the amino acid sequence (SEQ ID NO:190) derived from the coding sequence of SEQ ID NO:189 shown in Figure 69.

Figure 71 shows an EST nucleotide sequence designated herein as DNA43509 (SEQ ID NO:191).

Figure 72 shows a nucleotide sequence (SEQ ID NO:195) of a native sequence PRO852 cDNA, wherein

SEQ ID NO:195 is a clone designated herein as "UNQ418" and/or "DNA45493-1349".

Figure 73 shows the amino acid sequence (SEQ ID NO:196) derived from the coding sequence of SEQ ID NO:195 shown in Figure 72.

Figure 74 shows a nucleotide sequence (SEQ ID NO:205) of a native sequence PRO853 cDNA, wherein SEQ ID NO:205 is a clone designated herein as "UNQ419" and/or "DNA48227-1350".

Figure 75 shows the amino acid sequence (SEQ ID NO:206) derived from the coding sequence of SEQ ID NO:205 shown in Figure 74.

Figures 76A-B show a nucleotide sequence (SEQ ID NO:210) of a native sequence PRO860 cDNA, wherein SEQ ID NO:210 is a clone designated herein as "UNQ421" and/or "DNA41404-1352".

Figure 77 shows the amino acid sequence (SEQ ID NO:211) derived from the coding sequence of SEQ ID NO:210 shown in Figures 76A-B.

Figure 78 shows a nucleotide sequence (SEQ ID NO:215) of a native sequence PRO846 cDNA, wherein SEQ ID NO:215 is a clone designated herein as "UNQ422" and/or "DNA44196-1353".

Figure 79 shows the amino acid sequence (SEQ ID NO:216) derived from the coding sequence of SEQ ID NO:215 shown in Figure 78.

Figure 80 shows a nucleotide sequence (SEQ ID NO:220) of a native sequence PRO862 cDNA, wherein SEQ ID NO:220 is a clone designated herein as "UNQ424" and/or "DNA52187-1354".

Figure 81 shows the amino acid sequence (SEQ ID NO:221) derived from the coding sequence of SEQ ID NO:220 shown in Figure 80.

Figure 82 shows a nucleotide sequence (SEQ ID NO:225) of a native sequence PRO864 cDNA, wherein SEQ ID NO:225 is a clone designated herein as "UNQ426" and/or "DNA48328-1355".

Figure 83 shows the amino acid sequence (SEQ ID NO:226) derived from the coding sequence of SEQ ID NO:225 shown in Figure 82.

Figure 84 shows a nucleotide sequence (SEQ ID NO:230) of a native sequence PRO792 cDNA, wherein SEQ ID NO:230 is a clone designated herein as "UNQ431" and/or "DNA56352-1358".

Figure 85 shows the amino acid sequence (SEQ ID NO:231) derived from the coding sequence of SEQ ID NO:230 shown in Figure 84.

Figure 86 shows a nucleotide sequence (SEQ ID NO:235) of a native sequence PRO866 cDNA, wherein SEQ ID NO:235 is a clone designated herein as "UNQ435" and/or "DNA53971-1359".

Figure 87 shows the amino acid sequence (SEQ ID NO:236) derived from the coding sequence of SEQ ID NO:235 shown in Figure 86.

Figure 88 shows a nucleotide sequence (SEQ ID NO:244) of a native sequence PRO871 cDNA, wherein SEQ ID NO:244 is a clone designated herein as "UNQ438" and/or "DNA50919-1361".

Figure 89 shows the amino acid sequence (SEQ ID NO:245) derived from the coding sequence of SEQ ID NO:244 shown in Figure 88.

Figure 90 shows a nucleotide sequence (SEQ ID NO:253) of a native sequence PRO873 cDNA, wherein SEQ ID NO:253 is a clone designated herein as "UNQ440" and/or "DNA44179-1362".

Figure 91 shows the amino acid sequence (SEQ ID NO:254) derived from the coding sequence of SEQ ID NO:253 shown in Figure 90.

Figure 92 shows a nucleotide sequence (SEQ ID NO:258) of a native sequence PRO940 cDNA, wherein SEQ ID NO:258 is a clone designated herein as "UNQ477" and/or "DNA54002-1367".

Figure 93 shows the amino acid sequence (SEQ ID NO:259) derived from the coding sequence of SEQ ID NO:258 shown in Figure 92.

Figure 94 shows a nucleotide sequence (SEQ ID NO:263) of a native sequence PRO941 cDNA, wherein SEQ ID NO:263 is a clone designated herein as "UNQ478" and/or "DNA53906-1368".

Figure 95 shows the amino acid sequence (SEQ ID NO:264) derived from the coding sequence of SEQ ID NO:263 shown in Figure 94.

Figure 96 shows an EST nucleotide sequence designated herein as DNA6415 (SEQ ID NO:265).

Figure 97 shows a nucleotide sequence (SEQ ID NO:269) of a native sequence PRO944 cDNA, wherein SEQ ID NO:269 is a clone designated herein as "UNQ481" and/or "DNA52185-1370".

Figure 98 shows the amino acid sequence (SEQ ID NO:270) derived from the coding sequence of SEQ ID NO:269 shown in Figure 97.

Figure 99 shows an EST nucleotide sequence designated herein as DNA14007 (SEQ ID NO:271).

Figure 100 shows an EST nucleotide sequence designated herein as DNA12773 (SEQ ID NO:272).

Figure 101 shows an EST nucleotide sequence designated herein as DNA12746 (SEQ ID NO:273).

Figure 102 shows an EST nucleotide sequence designated herein as DNA12834 (SEQ ID NO:274).

Figure 103 shows an EST nucleotide sequence designated herein as DNA12846 (SEQ ID NO:275).

Figure 104 shows an EST nucleotide sequence designated herein as DNA13104 (SEQ ID NO:276).

Figure 105 shows an EST nucleotide sequence designated herein as DNA13259 (SEQ ID NO:277).

Figure 106 shows an EST nucleotide sequence designated herein as DNA13959 (SEQ ID NO:278).

Figure 107 shows an EST nucleotide sequence designated herein as DNA13961 (SEQ ID NO:279).

Figure 108 shows a nucleotide sequence (SEQ ID NO:283) of a native sequence PRO983 cDNA, wherein SEQ ID NO:283 is a clone designated herein as "UNQ484" and/or "DNA53977-1371".

Figure 109 shows the amino acid sequence (SEQ ID NO:284) derived from the coding sequence of SEQ ID NO:283 shown in Figure 108.

Figure 110 shows an EST nucleotide sequence designated herein as DNA17130 (SEQ ID NO:285).

Figure 111 shows an EST nucleotide sequence designated herein as DNA23466 (SEQ ID NO:286).

Figure 112 shows an EST nucleotide sequence designated herein as DNA26818 (SEQ ID NO:287).

Figure 113 shows an EST nucleotide sequence designated herein as DNA37618 (SEQ ID NO:288).

Figure 114 shows an EST nucleotide sequence designated herein as DNA41732 (SEQ ID NO:289).

Figure 115 shows an EST nucleotide sequence designated herein as DNA45980 (SEQ ID NO:290).

Figure 116 shows an EST nucleotide sequence designated herein as DNA46372 (SEQ ID NO:291).

Figure 117 shows a nucleotide sequence (SEQ ID NO:295) of a native sequence PRO1057 cDNA, wherein SEQ ID NO:295 is a clone designated herein as "UNQ522" and/or "DNA57253-1382".

Figure 118 shows the amino acid sequence (SEQ ID NO:296) derived from the coding sequence of SEQ ID NO:295 shown in Figure 117.

Figure 119 shows a nucleotide sequence (SEQ ID NO:300) of a native sequence PRO1071 cDNA, wherein SEQ ID NO:300 is a clone designated herein as "UNQ528" and/or "DNA58847-1383".

Figure 120 shows the amino acid sequence (SEQ ID NO:301) derived from the coding sequence of SEQ ID NO:300 shown in Figure 119.

Figure 121 shows a nucleotide sequence (SEQ ID NO:302) of a native sequence PRO1072 cDNA, wherein SEQ ID NO:302 is a clone designated herein as "UNQ529" and/or "DNA58747-1384".

Figure 122 shows the amino acid sequence (SEQ ID NO:303) derived from the coding sequence of SEQ ID NO:302 shown in Figure 121.

Figure 123 shows an EST nucleotide sequence designated herein as DNA40210 (SEQ ID NO:304).

Figure 124 shows a nucleotide sequence (SEQ ID NO:308) of a native sequence PRO1075 cDNA, wherein SEQ ID NO:308 is a clone designated herein as "UNQ532" and/or "DNA57689-1385".

Figure 125 shows the amino acid sequence (SEQ ID NO:309) derived from the coding sequence of SEQ ID NO:308 shown in Figure 124.

Figure 126 shows an EST nucleotide sequence designated herein as DNA13059 (SEQ ID NO:310).

Figure 127 shows an EST nucleotide sequence designated herein as DNA19463 (SEQ ID NO:311).

Figure 128 shows a nucleotide sequence (SEQ ID NO:321) of a native sequence PRO181 cDNA, wherein SEQ ID NO:321 is a clone designated herein as "UNQ155" and/or "DNA23330-1390".

Figure 129 shows the amino acid sequence (SEQ ID NO:322) derived from the coding sequence of SEQ ID NO:321 shown in Figure 128.

Figure 130 shows an EST nucleotide sequence designated herein as DNA13242 (SEQ ID NO:323).

Figure 131 shows a nucleotide sequence (SEQ ID NO:329) of a native sequence PRO195 cDNA, wherein SEQ ID NO:329 is a clone designated herein as "UNQ169" and/or "DNA26847-1395".

Figure 132 shows the amino acid sequence (SEQ ID NO:330) derived from the coding sequence of SEQ ID NO:329 shown in Figure 131.

Figure 133 shows an EST nucleotide sequence designated herein as DNA15062 (SEQ ID NO:331).

Figure 134 shows an EST nucleotide sequence designated herein as DNA13199 (SEQ ID NO:332).

Figure 135 shows a nucleotide sequence (SEQ ID NO:336) of a native sequence PRO865 cDNA, wherein SEQ ID NO:336 is a clone designated herein as "UNQ434" and/or "DNA53974-1401".

Figure 136 shows the amino acid sequence (SEQ ID NO:337) derived from the coding sequence of SEQ ID NO:336 shown in Figure 135.

Figure 137 shows an EST nucleotide sequence designated herein as DNA37642 (SEQ ID NO:338).

Figure 138 shows a nucleotide sequence (SEQ ID NO:345) of a native sequence PRO827 cDNA, wherein SEQ ID NO:345 is a clone designated herein as "UNQ468" and/or "DNA57039-1402".

Figure 139 shows the amino acid sequence (SEQ ID NO:346) derived from the coding sequence of SEQ ID NO:345 shown in Figure 138.

Figure 140 shows an EST nucleotide sequence designated herein as DNA47751 (SEQ ID NO:347).

Figure 141 shows a nucleotide sequence (SEQ ID NO:351) of a native sequence PRO1114 cDNA, wherein SEQ ID NO:351 is a clone designated herein as "UNQ557" and/or "DNA57033-1403".

Figure 142 shows the amino acid sequence (SEQ ID NO:352) derived from the coding sequence of SEQ ID NO:351 shown in Figure 141.

Figure 143 shows an EST nucleotide sequence designated herein as DNA48466 (SEQ ID NO:353).

Figure 144 shows a nucleotide sequence (SEQ ID NO:357) of a native sequence PRO237 cDNA, wherein SEQ ID NO:357 is a clone designated herein as "UNQ211" and/or "DNA34353-1428".

Figure 145 shows the amino acid sequence (SEQ ID NO:358) derived from the coding sequence of SEQ ID NO:357 shown in Figure 144.

Figure 146 shows a nucleotide sequence (SEQ ID NO:362) of a native sequence PRO541 cDNA, wherein SEQ ID NO:362 is a clone designated herein as "UNQ342" and/or "DNA45417-1432".

Figure 147 shows the amino acid sequence (SEQ ID NO:363) derived from the coding sequence of SEQ ID NO:362 shown in Figure 146.

Figure 148 shows a nucleotide sequence (SEQ ID NO:369) of a native sequence PRO273 cDNA, wherein SEQ ID NO:369 is a clone designated herein as "UNQ240" and/or "DNA39523-1192".

Figure 149 shows the amino acid sequence (SEQ ID NO:370) derived from the coding sequence of SEQ ID NO:369 shown in Figure 148.

Figure 150 shows a nucleotide sequence (SEQ ID NO:374) of a native sequence PRO701 cDNA, wherein SEQ ID NO:374 is a clone designated herein as "UNQ365" and/or "DNA44205-1285".

Figure 151 shows the amino acid sequence (SEQ ID NO:375) derived from the coding sequence of SEQ ID NO:374 shown in Figure 150.

Figure 152 shows a nucleotide sequence (SEQ ID NO:379) of a native sequence PRO704 cDNA, wherein SEQ ID NO:379 is a clone designated herein as "UNQ368" and/or "DNA50911-1288".

Figure 153 shows the amino acid sequence (SEQ ID NO:380) derived from the coding sequence of SEQ ID NO:379 shown in Figure 152.

Figure 154 shows a nucleotide sequence (SEQ ID NO:384) of a native sequence PRO706 cDNA, wherein SEQ ID NO:384 is a clone designated herein as "UNQ370" and/or "DNA48329-1290".

Figure 155 shows the amino acid sequence (SEQ ID NO:385) derived from the coding sequence of SEQ ID NO:384 shown in Figure 154.

Figure 156 shows a nucleotide sequence (SEQ ID NO:389) of a native sequence PRO707 cDNA, wherein SEQ ID NO:389 is a clone designated herein as "UNQ371" and/or "DNA48306-1291".

Figure 157 shows the amino acid sequence (SEQ ID NO:390) derived from the coding sequence of SEQ ID NO:389 shown in Figure 156.

Figure 158 shows a nucleotide sequence (SEQ ID NO:394) of a native sequence PRO322 cDNA, wherein SEQ ID NO:394 is a clone designated herein as "UNQ283" and/or "DNA48336-1309".

Figure 159 shows the amino acid sequence (SEQ ID NO:395) derived from the coding sequence of SEQ

ID NO:394 shown in Figure 158.

Figure 160 shows a nucleotide sequence (SEQ ID NO:399) of a native sequence PRO526 cDNA, wherein SEQ ID NO:399 is a clone designated herein as "UNQ330" and/or "DNA44184-1319".

Figure 161 shows the amino acid sequence (SEQ ID NO:400) derived from the coding sequence of SEQ ID NO:399 shown in Figure 160.

Figure 162 shows a nucleotide sequence (SEQ ID NO:404) of a native sequence PRO531 cDNA, wherein SEQ ID NO:404 is a clone designated herein as "UNQ332" and/or "DNA48314-1320".

Figure 163 shows the amino acid sequence (SEQ ID NO:405) derived from the coding sequence of SEQ ID NO:404 shown in Figure 162.

Figure 164 shows a nucleotide sequence (SEQ ID NO:409) of a native sequence PRO534 cDNA, wherein SEQ ID NO:409 is a clone designated herein as "UNQ335" and/or "DNA48333-1321".

Figure 165 shows the amino acid sequence (SEQ ID NO:410) derived from the coding sequence of SEQ ID NO:409 shown in Figure 164.

Figure 166 shows a nucleotide sequence (SEQ ID NO:414) of a native sequence PRO697 cDNA, wherein SEQ ID NO:414 is a clone designated herein as "UNQ361" and/or "DNA50920-1325".

Figure 167 shows the amino acid sequence (SEQ ID NO:415) derived from the coding sequence of SEQ ID NO:414 shown in Figure 166.

Figure 168 shows a nucleotide sequence (SEQ ID NO:419) of a native sequence PRO717 cDNA, wherein SEQ ID NO:419 is a clone designated herein as "UNQ385" and/or "DNA50988-1326".

Figure 169 shows the amino acid sequence (SEQ ID NO:420) derived from the coding sequence of SEQ ID NO:419 shown in Figure 168.

Figures 170A-B show a nucleotide sequence (SEQ ID NO:424) of a native sequence PRO731 cDNA, wherein SEQ ID NO:424 is a clone designated herein as "UNQ395" and/or "DNA48331-1329".

Figure 171 shows the amino acid sequence (SEQ ID NO:425) derived from the coding sequence of SEQ ID NO:424 shown in Figures 170A-B.

Figure 172 shows a nucleotide sequence (SEQ ID NO:429) of a native sequence PRO218 cDNA, wherein SEQ ID NO:429 is a clone designated herein as "UNQ192" and/or "DNA30867-1335".

Figure 173 shows the amino acid sequence (SEQ ID NO:430) derived from the coding sequence of SEQ ID NO:429 shown in Figure 172.

Figure 174 shows an EST nucleotide sequence designated herein as DNA14472 (SEQ ID NO:431).

Figure 175 shows an EST nucleotide sequence designated herein as DNA15846 (SEQ ID NO:432).

Figures 176A-B show a nucleotide sequence (SEQ ID NO:436) of a native sequence PRO768 cDNA, wherein SEQ ID NO:436 is a clone designated herein as "UNQ406" and/or "DNA55737-1345".

Figure 177 shows the amino acid sequence (SEQ ID NO:437) derived from the coding sequence of SEQ ID NO:436 shown in Figures 176A-B.

Figure 178 shows a nucleotide sequence (SEQ ID NO:441) of a native sequence PRO771 cDNA, wherein SEQ ID NO:441 is a clone designated herein as "UNQ409" and/or "DNA49829-1346".

Figure 179 shows the amino acid sequence (SEQ ID NO:442) derived from the coding sequence of SEQ ID NO:441 shown in Figure 178.

Figures 180A-B show a nucleotide sequence (SEQ ID NO:446) of a native sequence PRO733 cDNA, wherein SEQ ID NO:446 is a clone designated herein as "UNQ411" and/or "DNA52196-1348".

Figure 181 shows the amino acid sequence (SEQ ID NO:447) derived from the coding sequence of SEQ ID NO:446 shown in Figures 180A-B.

Figure 182 shows a nucleotide sequence (SEQ ID NO:451) of a native sequence PRO162 cDNA, wherein SEQ ID NO:451 is a clone designated herein as "UNQ429" and/or "DNA46965-1356".

Figure 183 shows the amino acid sequence (SEQ ID NO:452) derived from the coding sequence of SEQ ID NO:451 shown in Figure 182.

Figure 184 shows a nucleotide sequence (SEQ ID NO:453) of a native sequence PRO788 cDNA, wherein SEQ ID NO:453 is a clone designated herein as "UNQ430" and/or "DNA56405-1357".

Figure 185 shows the amino acid sequence (SEQ ID NO:454) derived from the coding sequence of SEQ ID NO:453 shown in Figure 184.

Figure 186 shows a nucleotide sequence (SEQ ID NO:455) of a native sequence PRO1008 cDNA, wherein SEQ ID NO:455 is a clone designated herein as "UNQ492" and/or "DNA57530-1375".

Figure 187 shows the amino acid sequence (SEQ ID NO:456) derived from the coding sequence of SEQ ID NO:455 shown in Figure 186.

Figure 188 shows an EST nucleotide sequence designated herein as DNA16508 (SEQ ID NO:457).

Figures 189A-B show a nucleotide sequence (SEQ ID NO:458) of a native sequence PRO1012 cDNA, wherein SEQ ID NO:458 is a clone designated herein as "UNQ495" and/or "DNA56439-1376".

Figure 190 shows the amino acid sequence (SEQ ID NO:459) derived from the coding sequence of SEQ ID NO:458 shown in Figures 189A-B.

Figure 191 shows a nucleotide sequence (SEQ ID NO:463) of a native sequence PRO1014 cDNA, wherein SEQ ID NO:463 is a clone designated herein as "UNQ497" and/or "DNA56409-1377".

Figure 192 shows the amino acid sequence (SEQ ID NO:464) derived from the coding sequence of SEQ ID NO:463 shown in Figure 191.

Figure 193 shows a nucleotide sequence (SEQ ID NO:465) of a native sequence PRO1017 cDNA, wherein SEQ ID NO:465 is a clone designated herein as "UNQ500" and/or "DNA56112-1379".

Figure 194 shows the amino acid sequence (SEQ ID NO:466) derived from the coding sequence of SEQ ID NO:465 shown in Figure 193.

Figure 195 shows a nucleotide sequence (SEQ ID NO:467) of a native sequence PRO474 cDNA, wherein SEQ ID NO:467 is a clone designated herein as "UNQ502" and/or "DNA56045-1380".

Figure 196 shows the amino acid sequence (SEQ ID NO:468) derived from the coding sequence of SEQ ID NO:467 shown in Figure 195.

Figure 197 shows a nucleotide sequence (SEQ ID NO:469) of a native sequence PRO1031 cDNA, wherein SEQ ID NO:469 is a clone designated herein as "UNQ516" and/or "DNA59294-1381".

Figure 198 shows the amino acid sequence (SEQ ID NO:470) derived from the coding sequence of SEQ ID NO:469 shown in Figure 197.

Figure 199 shows a nucleotide sequence (SEQ ID NO:471) of a native sequence PRO938 cDNA, wherein SEQ ID NO:471 is a clone designated herein as "UNQ475" and/or "DNA56433-1406".

Figure 200 shows the amino acid sequence (SEQ ID NO:472) derived from the coding sequence of SEQ ID NO:471 shown in Figure 199.

Figure 201 shows a nucleotide sequence (SEQ ID NO:476) of a native sequence PRO1082 cDNA, wherein SEQ ID NO:476 is a clone designated herein as "UNQ539" and/or "DNA53912-1457".

Figure 202 shows the amino acid sequence (SEQ ID NO:477) derived from the coding sequence of SEQ ID NO:476 shown in Figure 201.

Figure 203 shows a nucleotide sequence (SEQ ID NO:482) of a native sequence PRO1083 cDNA, wherein SEQ ID NO:482 is a clone designated herein as "UNQ540" and/or "DNA50921-1458".

Figure 204 shows the amino acid sequence (SEQ ID NO:483) derived from the coding sequence of SEQ ID NO:482 shown in Figure 203.

Figure 205 shows an EST nucleotide sequence designated herein as DNA24256 (SEQ ID NO:484).

Figure 206 shows a nucleotide sequence (SEQ ID NO:487) of a native sequence PRO200 cDNA, wherein SEQ ID NO:487 is a clone designated herein as "UNQ174" and/or "DNA29101-1122".

Figure 207 shows the amino acid sequence (SEQ ID NO:488) derived from the coding sequence of SEQ ID NO:487 shown in Figure 206.

Figure 208 shows a nucleotide sequence (SEQ ID NO:495) of a native sequence PRO285 cDNA, wherein SEQ ID NO:495 is a clone designated herein as "DNA40021-1154".

Figure 209 shows the amino acid sequence (SEQ ID NO:496) derived from the coding sequence of SEQ ID NO:495 shown in Figure 208.

Figures 210A-B show a nucleotide sequence (SEQ ID NO:497) of a native sequence PRO286 cDNA, wherein SEQ ID NO:497 is a clone designated herein as "DNA42663-1154".

Figure 211 shows the amino acid sequence (SEQ ID NO:498) derived from the coding sequence of SEQ ID NO:497 shown in Figures 210A-B.

Figure 212 shows a nucleotide sequence (SEQ ID NO:505) of a native sequence PRO213-1 cDNA, wherein SEQ ID NO:505 is a clone designated herein as "DNA30943-1-1163-1".

Figure 213 shows the amino acid sequence (SEQ ID NO:506) derived from the coding sequence of SEQ ID NO:505 shown in Figure 212.

Figure 214 shows a nucleotide sequence (SEQ ID NO:507) of a native sequence PRO1330 cDNA, wherein SEQ ID NO:507 is a clone designated herein as "DNA64907-1163-1".

Figure 215 shows the amino acid sequence (SEQ ID NO:508) derived from the coding sequence of SEQ ID NO:507 shown in Figure 214.

Figure 216 shows a nucleotide sequence (SEQ ID NO:509) of a native sequence PRO1449 cDNA, wherein SEQ ID NO:509 is a clone designated herein as "DNA64908-1163-1".

Figure 217 shows the amino acid sequence (SEQ ID NO:510) derived from the coding sequence of SEQ ID NO:509 shown in Figure 216.

Figure 218 shows a nucleotide sequence (SEQ ID NO:514) of a native sequence PRO298 cDNA, wherein SEQ ID NO:514 is a clone designated herein as "UNQ261" and/or "DNA39975-1210".

Figure 219 shows the amino acid sequence (SEQ ID NO:515) derived from the coding sequence of SEQ ID NO:514 shown in Figure 218.

Figure 220 shows an EST nucleotide sequence designated herein as DNA26832 (SEQ ID NO:516).

Figure 221 shows a nucleotide sequence (SEQ ID NO:522) of a native sequence PRO337 cDNA, wherein SEQ ID NO:522 is a clone designated herein as "DNA43316-1237".

Figure 222 shows the amino acid sequence (SEQ ID NO:523) derived from the coding sequence of SEQ ID NO:522 shown in Figure 221.

Figure 223 shows an EST nucleotide sequence designated herein as DNA42301 (SEQ ID NO:524).

Figure 224 shows a nucleotide sequence (SEQ ID NO:525) of a native sequence PRO403 cDNA, wherein SEQ ID NO:525 is a clone designated herein as "DNA55800-1263".

Figure 225 shows the amino acid sequence (SEQ ID NO:526) derived from the coding sequence of SEQ ID NO:525 shown in Figure 224.

Figures 226A-B show an EST nucleotide sequence designated herein as DNA34415 (SEQ ID NO:527).

Figure 227 shows an EST nucleotide sequence designated herein as DNA49830 (SEQ ID NO:528).

Figure 228 shows an EST nucleotide sequence designated herein as DNA49831 (SEQ ID NO:529).

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and "PRO/number" as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods.

A "native sequence PRO polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (*e.g.*, an extracellular domain sequence), naturally-occurring variant forms (*e.g.*, alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO213 polypeptide is a mature or full-length native sequence PRO213 polypeptide comprising amino acids 1 to 295 of Figure 2 (SEQ ID NO:2), the native sequence PRO274 polypeptide is a mature or full-length native sequence PRO274 polypeptide comprising amino acids 1 to 492

of Figure 4 (SEQ ID NO:7), the native sequence PRO300 polypeptide is a mature or full-length native sequence PRO300 polypeptide comprising amino acids 1 to 457 of Figure 9 (SEQ ID NO:19), the native sequence PRO284 polypeptide is a mature or full-length native sequence PRO284 polypeptide comprising amino acids 1 to 285 of Figure 11 (SEQ ID NO:28), the native sequence PRO296 polypeptide is a mature or full-length native sequence PRO296 polypeptide comprising amino acids 1 to 204 of Figure 15 (SEQ ID NO:36), the native sequence PRO329 polypeptide is a mature or full-length native sequence PRO329 polypeptide comprising amino acids 1 to 359 of Figure 20 (SEQ ID NO:45), the native sequence PRO362 polypeptide is a mature or full-length native sequence PRO362 polypeptide comprising amino acids 1 to 321 of Figure 22 (SEQ ID NO:52), the native sequence PRO363 polypeptide is a mature or full-length native sequence PRO363 polypeptide comprising amino acids 1 to 373 of Figure 24 (SEQ ID NO:59), the native sequence PRO868 polypeptide is a mature or full-length native sequence PRO868 polypeptide comprising amino acids 1 to 655 of Figure 26 (SEQ ID NO:64), the native sequence PRO382 polypeptide is a mature or full-length native sequence PRO382 polypeptide comprising amino acids 1 to 453 of Figure 28 (SEQ ID NO:69), the native sequence PRO545 polypeptide is a mature or full-length native sequence PRO545 polypeptide comprising amino acids 1 to 735 of Figure 30 (SEQ ID NO:74), the native sequence PRO617 polypeptide is a mature or full-length native sequence PRO617 polypeptide comprising amino acids 1 to 67 of Figure 33 (SEQ ID NO:85), the native sequence PRO700 polypeptide is a mature or full-length native sequence PRO700 polypeptide comprising amino acids 1 to 432 of Figure 35 (SEQ ID NO:90), the native sequence PRO702 polypeptide is a mature or full-length native sequence PRO702 polypeptide comprising amino acids 1 to 277 of Figure 37 (SEQ ID NO:97), the native sequence PRO703 polypeptide is a mature or full-length native sequence PRO703 polypeptide comprising amino acids 1 to 730 of Figure 39 (SEQ ID NO:102), the native sequence PRO705 polypeptide is a mature or full-length native sequence PRO705 polypeptide comprising amino acids 1 to 555 of Figure 41 (SEQ ID NO:109), the native sequence PRO708 polypeptide is a mature or full-length native sequence PRO708 polypeptide comprising amino acids 1 to 515 of Figure 43 (SEQ ID NO:114), the native sequence PRO320 polypeptide is a mature or full-length native sequence PRO320 polypeptide comprising amino acids 1 to 338 of Figure 45 (SEQ ID NO:119), the native sequence PRO324 polypeptide is a mature or full-length native sequence PRO324 polypeptide comprising amino acids 1 to 289 of Figure 47 (SEQ ID NO:124), the native sequence PRO351 polypeptide is a mature or full-length native sequence PRO351 polypeptide comprising amino acids 1 to 571 of Figure 49 (SEQ ID NO:132), the native sequence PRO352 polypeptide is a mature or full-length native sequence PRO352 polypeptide comprising amino acids 1 to 316 of Figure 51 (SEQ ID NO:137), the native sequence PRO381 polypeptide is a mature or full-length native sequence PRO381 polypeptide comprising amino acids 1 to 211 of Figure 53 (SEQ ID NO:145), the native sequence PRO386 polypeptide is a mature or full-length native sequence PRO386 polypeptide comprising amino acids 1 to 215 of Figure 55 (SEQ ID NO:150), the native sequence PRO540 polypeptide is a mature or full-length native sequence PRO540 polypeptide comprising amino acids 1 to 412 of Figure 59 (SEQ ID NO:157), the native sequence PRO615 polypeptide is a mature or full-length native sequence PRO615 polypeptide comprising amino acids 1 to 224 of Figure 61 (SEQ ID NO:162), the native sequence PRO618 polypeptide is a mature or full-length native sequence PRO618 polypeptide comprising amino acids 1 to 802 of

Figure 63 (SEQ ID NO:169), the native sequence PRO719 polypeptide is a mature or full-length native sequence PRO719 polypeptide comprising amino acids 1 to 354 of Figure 66 (SEQ ID NO:178), the native sequence PRO724 polypeptide is a mature or full-length native sequence PRO724 polypeptide comprising amino acids 1 to 713 of Figure 68 (SEQ ID NO:183), the native sequence PRO772 polypeptide is a mature or full-length native sequence PRO772 polypeptide comprising amino acids 1 to 152 of Figure 70 (SEQ ID NO:190), the native sequence PRO852 polypeptide is a mature or full-length native sequence PRO852 polypeptide comprising amino acids 1 to 518 of Figure 73 (SEQ ID NO:196), the native sequence PRO853 polypeptide is a mature or full-length native sequence PRO853 polypeptide comprising amino acids 1 to 377 of Figure 75 (SEQ ID NO:206), the native sequence PRO860 polypeptide is a mature or full-length native sequence PRO860 polypeptide comprising amino acids 1 to 985 of Figure 77 (SEQ ID NO:211), the native sequence PRO846 polypeptide is a mature or full-length native sequence PRO846 polypeptide comprising amino acids 1 to 332 of Figure 79 (SEQ ID NO:216), the native sequence PRO862 polypeptide is a mature or full-length native sequence PRO862 polypeptide comprising amino acids 1 to 146 of Figure 81 (SEQ ID NO:221), the native sequence PRO864 polypeptide is a mature or full-length native sequence PRO864 polypeptide comprising amino acids 1 to 351 of Figure 83 (SEQ ID NO:226), the native sequence PRO792 polypeptide is a mature or full-length native sequence PRO792 polypeptide comprising amino acids 1 to 293 of Figure 85 (SEQ ID NO:231), the native sequence PRO866 polypeptide is a mature or full-length native sequence PRO866 polypeptide comprising amino acids 1 to 331 of Figure 87 (SEQ ID NO:236), the native sequence PRO871 polypeptide is a mature or full-length native sequence PRO871 polypeptide comprising amino acids 1 to 472 of Figure 89 (SEQ ID NO:245), the native sequence PRO873 polypeptide is a mature or full-length native sequence PRO873 polypeptide comprising amino acids 1 to 545 of Figure 91 (SEQ ID NO:254), the native sequence PRO940 polypeptide is a mature or full-length native sequence PRO940 polypeptide comprising amino acids 1 to 544 of Figure 93 (SEQ ID NO:259), the native sequence PRO941 polypeptide is a mature or full-length native sequence PRO941 polypeptide comprising amino acids 1 to 772 of Figure 95 (SEQ ID NO:264), the native sequence PRO944 polypeptide is a mature or full-length native sequence PRO944 polypeptide comprising amino acids 1 to 211of Figure 98 (SEQ ID NO:270), the native sequence PRO983 polypeptide is a mature or full-length native sequence PRO983 polypeptide comprising amino acids 1 to 243 of Figure 109 (SEQ ID NO:284), the native sequence PRO1057 polypeptide is a mature or full-length native sequence PRO1057 polypeptide comprising amino acids 1 to 413 of Figure 118 (SEQ ID NO:296), the native sequence PRO1071 polypeptide is a mature or full-length native sequence PRO1071 polypeptide comprising amino acids 1 to 525 of Figure 120 (SEQ ID NO:301), the native sequence PRO1072 polypeptide is a mature or full-length native sequence PRO1072 polypeptide comprising amino acids 1 to 336 of Figure 122 (SEQ ID NO:303), the native sequence PRO1075 polypeptide is a mature or full-length native sequence PRO1075 polypeptide comprising amino acids 1 to 406 of Figure 125 (SEQ ID NO:309), the native sequence PRO181 polypeptide is a mature or full-length native sequence PRO181 polypeptide comprising amino acids 1 to 144 of Figure 129 (SEQ ID NO:322), the native sequence PRO195 polypeptide is a mature or full-length native sequence PRO195 polypeptide comprising amino acids 1 to 323 of Figure 132 (SEQ ID NO:330), the native sequence PRO865 polypeptide is a mature or full-length native

sequence PRO865 polypeptide comprising amino acids 1 to 468 of Figure 136 (SEQ ID NO:337), the native sequence PRO827 polypeptide is a mature or full-length native sequence PRO827 polypeptide comprising amino acids 1 to 124 of Figure 39 (SEQ ID NO:346), the native sequence PRO1114 polypeptide is a mature or full-length native sequence PRO1114 polypeptide comprising amino acids 1 to 311 of Figure 142 (SEQ ID NO:352), the native sequence PRO237 polypeptide is a mature or full-length native sequence PRO237 polypeptide comprising amino acids 1 to 328 of Figure 145 (SEQ ID NO:358), the native sequence PRO541 polypeptide is a mature or full-length native sequence PRO541 polypeptide comprising amino acids 1 to 500 of Figure 147 (SEQ ID NO:363), the native sequence PRO273 polypeptide is a mature or full-length native sequence PRO273 polypeptide comprising amino acids 1 through 111 of Figure 149 (SEQ ID NO:370), the native sequence PRO701 polypeptide is a mature or full-length native sequence PRO701 polypeptide comprising amino acids 1 to 816 of Figure 151 (SEQ ID NO:375), the native sequence PRO704 polypeptide is a full-length or mature native sequence PRO704 polypeptide comprising amino acids 1 or 40 through 348 of Figure 153 (SEQ ID NO:380), the native sequence PRO706 polypeptide is a mature or full-length native sequence PRO706 polypeptide comprising amino acids 1 to 480 of Figure 155 (SEQ ID NO:385), the native sequence PRO707 polypeptide is a full-length or mature native sequence PRO707 polypeptide comprising amino acids 1 or 31 through 916 of Figure 157 (SEQ ID NO:390), the native sequence PRO322 polypeptide is a mature or full-length native sequence PRO322 polypeptide comprising amino acids 24 or 1 to 260 of Figure 159 (SEQ ID NO:395), the native sequence PRO526 polypeptide is a full-length or mature native sequence PRO526 polypeptide comprising amino acids 1 or 27 through 473 of Figure 161 (SEQ ID NO:400), the native sequence PRO531 polypeptide is a mature PRO531 polypeptide comprising amino acids 1 to 789 of Figure 163 (SEQ ID NO:405), the native sequence PRO534 polypeptide is a mature or full-length native sequence PRO534 polypeptide comprising amino acids 1 to 360 of Figure 165 (SEQ ID NO:410), the native sequence PRO697 polypeptide is a full-length or mature native sequence PRO697 polypeptide comprising amino acids 1 or 21 through 295 of Figure 167 (SEQ ID NO:415), the native sequence PRO717 polypeptide is a mature or full-length native sequence PRO717 polypeptide comprising amino acids 1 through 560 of Figure 169 (SEQ ID NO:420), the native sequence PRO731 polypeptide is a full-length or mature native sequence PRO731 polypeptide comprising amino acids 1 or 14 through 1184 of Figure 171 (SEQ ID NO:425), the native sequence PRO218 polypeptide is a full-length or mature native sequence PRO218 polypeptide comprising amino acids 1 or 24 through 455 of Figure 173 (SEQ ID NO:430), the native sequence PRO768 polypeptide is a full-length or mature native sequence PRO768 polypeptide comprising amino acids 1 or 34 through 1141 of Figure 177 (SEQ ID NO:437), the native sequence PRO771 polypeptide is a full-length or mature native sequence PRO771 polypeptide comprising amino acids 1 or 17 through 436 of Figure 179 (SEQ ID NO:442), the native sequence PRO733 polypeptide is a mature or full-length native sequence PRO733 polypeptide comprising amino acids 24 or 1 through 229 of Figure 181 (SEQ ID NO:447), the native sequence PRO162 polypeptide is a full-length or mature native sequence PRO162 polypeptide comprising amino acids 1 or 27 through 175 of Figure 183 (SEQ ID NO:452), the native sequence PRO788 polypeptide is a full-length or mature native sequence PRO788 polypeptide comprising amino acids 1 or 18 through 125 of Figure 185 (SEQ ID NO:454), the native sequence

PRO1008 polypeptide is a full-length or mature native sequence PRO1008 polypeptide comprising amino acids 1 or 24 through 266 of Figure 187 (SEQ ID NO:456), the native sequence PRO1012 polypeptide is a mature or full-length native sequence PRO1012 polypeptide comprising amino acids 1 through 747 of Figure 190 (SEQ ID NO:459), the native sequence PRO1014 polypeptide is a full-length or mature native sequence PRO1014 polypeptide comprising amino acids 1 or 20 through 300 of Figure 192 (SEQ ID NO:464), the native sequence PRO1017 polypeptide is a full-length or mature native sequence PRO1017 polypeptide comprising amino acids 1 or 32 through 414 of Figure 194 (SEQ ID NO:466), the native sequence PRO474 polypeptide is a mature or full-length native sequence PRO474 polypeptide comprising amino acids 1 through 270 of Figure 196 (SEQ ID NO:468), the native sequence PRO1031 polypeptide is a full-length or mature native sequence PRO1031 polypeptide comprising amino acids 1 or 21 through 180 of Figure 198 (SEQ ID NO:470), the native sequence PRO938 polypeptide is a mature or full-length native sequence PRO938 polypeptide comprising amino acids 1 to 349 of Figure 200 (SEQ ID NO:472), the native sequence PRO1082 polypeptide is a full-length or mature native sequence PRO1082 polypeptide comprising amino acids 1 through 201 of Figure 202 (SEQ ID NO:477), the native sequence PRO1083 polypeptide is a full-length or mature native sequence PRO1083 polypeptide comprising amino acids 1 or 26 through 693 of Figure 204 (SEQ ID NO:483), the native sequence VEGF-E polypeptide is a mature or full-length native sequence VEGF-E polypeptide comprising amino acids 1 through 345 as depicted in Figure 207 (SEQ ID NO:488), the native sequence PRO285 is a mature or full-length native sequence PRO285 polypeptide comprising amino acids 1 to 1049 of Figure 209 (SEQ ID NO:496), the native sequence PRO286 is a mature or full-length native sequence PRO286 polypeptide comprising amino acids 1 to 1041 of Figure 211 (SEQ ID NO:298), the native sequence PRO298 is a mature or full-length native sequence PRO298 comprising amino acids 1 to 364 of Figure 219 (SEQ ID NO:515), the native sequence PRO337 is a mature or full-length native sequence human neurotrimin comprising amino acids 1 to 344 of Figure 222 (SEQ ID NO:523), with or without the N-terminal signal sequence (residues 1 to about 28), and with or without the initiating methionine at position 1 and the native sequence PRO403 is a mature or full-length native sequence comprising amino acids 1 to 736 of Figure 225 (SEQ ID NO:526), with or without the initiating methionine at position 1.

The PRO polypeptide "extracellular domain" or "ECD" refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either or the transmembrane domain as initially identified.

"PRO polypeptide variant" means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with the full-length native sequence PRO polypeptide sequence as

disclosed herein. Such PRO polypeptide variants include, for instance, PRO polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, more preferably at least about 85% amino acid sequence identity, and even more preferably at least about 90% amino acid sequence identity, even more preferably at least about 91% amino acid sequence identity, even more preferably at least about 92% amino acid sequence identity, even more preferably at least about 93% amino acid sequence identity, even more preferably at least about 94% amino acid sequence identity, even more preferably at least about 95% amino acid sequence identity, yet more preferably at least about 96% amino acid sequence identity, yet more preferably at least about 97% amino acid sequence identity, yet more preferably at least about 98% amino acid sequence identity and most preferably at least about 99% amino acid sequence identity with the amino acid sequence of the full-length native amino acid sequence as disclosed herein.

"Percent (%) amino acid sequence identity" with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. The preferred software alignment program is BLAST. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. The % identity values used herein have been generated using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996); http://blast.wustl/edu/blast/README.html). Most of the WU-BLAST-2 search parameters were set to the default values. The adjustable parameters were set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. The HSP S and HSP S2 parameters, which are dynamic values used by BLAST-2, are established by the program itself depending upon the composition of the sequence of interest and composition of the database against which the sequence is being searched. However, the values may be adjusted to increase sensitivity. A % sequence identity value is determined by the fraction of matching identical residues divided by the total number of residues in the aligned region.

"Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any

algorithms needed to achieve maximal alignment over the full length of the sequences being compared. The identity values used herein were generated by the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.

The term "positives", in the context of sequence comparison performed as described above, includes residues in the sequences compared that are not identical but have similar properties (e.g. as a result of conservative substitutions). The % value of positives is determined by the fraction of residues scoring a positive value in the BLOSUM 62 matrix divided by the total number of residues in the aligned region, as defined above.

The term "epitope tagged" where used herein refers to a chimeric polypeptide comprising a PRO polypeptide, or domain sequence thereof, fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody may be made, or which can be identified by some other agent, yet is short enough such that it does not interfere with the activity of the PRO polypeptide of interest.. The tag polypeptide preferably is also fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 to about 50 amino acid residues (preferably, between about 10 to about 20 residues).

"Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" PRO polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the PRO polypeptide nucleic acid. An isolated PRO polypeptide nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated PRO polypeptide nucleic acid molecules therefore are distinguished from the specific PRO polypeptide nucleic acid molecule as it exists in natural cells. However, an isolated PRO polypeptide nucleic acid molecule includes PRO polypeptide nucleic acid molecules contained in cells that ordinarily express the PRO polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic

acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The term "antibody" is used in the broadest sense and specifically covers single anti-PRO polypeptide monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies) and anti-PRO polypeptide antibody compositions with polyepitopic specificity. The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

"Active" or "activity" for the purposes herein refers to form(s) of PRO polypeptide which retain the biologic and/or immunologic activities of the specific native or naturally-occurring PRO polypeptide.

"Treatment" or "treating" refers to both therapeutic treatment and prophylactic or preventative measures. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in which the disorder is to be prevented.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as sheep, dogs, horses, cats, cows, and the like. Preferably, the mammal herein is a human.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

The term "agonist" is used to refer to peptide and non-peptide analogs of the native PRO polypeptides (where native PRO polypeptide refers to pro-PRO polypeptide, pre-PRO polypeptide, prepro-PRO polypeptide, or mature PRO polypeptide) of the present invention and to antibodies specifically binding such native PRO polypeptides, provided that they retain at least one biological activity of a native PRO polypeptide. Preferably, the agonists of the present invention retain the qualitative binding recognition properties and receptor activation

properties of the native PRO polypeptide.

The term "antagonist" is used to refer to a molecule inhibiting a biological activity of a native PRO polypeptide of the present invention wherein native PRO polypeptide refers to pro-PRO polypeptide, pre-PRO polypeptide, prepro-PRO polypeptide, or mature PRO polypeptide. Preferably, the antagonists herein inhibit the binding of a native PRO polypeptide of the present invention to a binding partner. A PRO polypeptide "antagonist" is a molecule which prevents, or interferes with, a PRO antagonist effector function (*e.g.* a molecule which prevents or interferes with binding and/or activation of a PRO polypeptide receptor by PRO polypeptide). Such molecules can be screened for their ability to competitively inhibit PRO polypeptide receptor activation by monitoring binding of native PRO polypeptide in the presence and absence of the test antagonist molecule, for example. An antagonist of the invention also encompasses an antisense polynucleotide against the PRO polypeptide gene, which antisense polynucleotide blocks transcription or translation of the PRO polypeptide gene, thereby inhibiting its expression and biological activity.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel *et al.*, Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" means (1) employing low ionic strength and high temperature for washing, for example, 0.015 sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C, or (2) employing during hybridization a denaturing agent, such as formamide, for example, 50% (vol/vol) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 nM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C. Another example is use of 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6/8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 μg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC and 0.1% SDS. Yet another example is hybridization using a buffer of 10% dextran sulfate, 2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" are described in Sambrook *et al.*, *supra*, and include the use of a washing solution and hybridization conditions (*e.g.*, temperature, ionic strength, and %SDS) less stringent than described above. An example of moderately stringent conditions is a condition such as overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/mL denatured sheared

salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, *etc.*, as necessary to accommodate factors such as probe length and the like.

"Southern analysis" or "Southern blotting" is a method by which the presence of DNA sequences in a restriction endonuclease digest of DNA or a DNA-containing composition is confirmed by hybridization to a known, labeled oligonucleotide or DNA fragment. Southern analysis typically involves electrophoretic separation of DNA digests on agarose gels, denaturation of the DNA after electrophoretic separation, and transfer of the DNA to nitrocellulose, nylon, or another suitable membrane support for analysis with a radiolabeled, biotinylated, or enzyme-labeled probe as described in sections 9.37-9.52 of Sambrook *et al.*, Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989).

"Northern analysis" or "Northern blotting" is a method used to identify RNA sequences that hybridize to a known probe such as an oligonucleotide, DNA fragment, cDNA or fragment thereof, or RNA fragment. The probe is labeled with a radioisotope such as ^{32}P, or by biotinylation, or with an enzyme. The RNA to be analyzed is usually electrophoretically separated on an agarose or polyacrylamide gel, transferred to nitrocellulose, nylon, or other suitable membrane, and hybridized with the probe, using standard techniques well known in the art such as those described in sections 7.39-7.52 of Sambrook *et al., supra*.

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

As used herein, "vascular endothelial cell growth factor-E," or "VEGF-E," refers to a mammalian growth factor as described herein, including the human amino acid sequence of Figure 207, a sequence which has homology to VEGF and bone morphogenetic protein 1 and which includes complete conservation of all VEGF cysteine residues, which have been shown to be required for biological activity of VEGF. VEGF-E expression includes expression in human fetal bone, thymus, and the gastrointestinal tract. The biological activity of native VEGF-E is shared by any analogue or variant thereof that is capable of promoting selective

growth and/or survival of umbilical vein endothelial cells, induces proliferation of pluripotent fibroblast cells, induces immediate early gene c-fos in human endothelial cell lines and causes myocyte hypertrophy in cardiac cells, or which possesses an immune epitope that is immunologically cross-reactive with an antibody raised against at least one epitope of the corresponding native VEGF-E. The human VEGF-E herein is active on rat and mouse cells indicating conservation across species. Moreover, the VEGF-E herein is expressed at the growth plate region and has been shown to embrace fetal myocytes.

As used herein, "vascular endothelial cell growth factor," or "VEGF," refers to a mammalian growth factor as defined in U.S. Patent 5,332,671. The biological activity of native VEGF is shared by any analogue or variant thereof that is capable of promoting selective growth of vascular endothelial cells but not of bovine corneal endothelial cells, lens epithelial cells, adrenal cortex cells, BHK-21 fibroblasts, or keratinocytes, or that possesses an immune epitope that is immunologically cross-reactive with an antibody raised against at least one epitope of the corresponding native VEGF.

The terms "VEGF-E polypeptide" and "VEGF-E" when used herein encompass native sequence VEGF-E polypeptide and VEGF-E polypeptide variants (which are further defined herein). The VEGF-E polypeptides may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods.

Inhibitors of VEGF-E include those which reduce or inhibit the activity or expression of VEGF-E and includes antisense molecules.

The abbreviation "KDR" refers to the kinase domain region of the VEGF molecule. VEGF-E has no homology with VEGF in this domain.

The abbreviation "FLT-1" refers to the FMS-like tyrosine kinase binding domain which is known to bind to the corresponding FLT-1 receptor. VEGF-E has no homology with VEGF in this domain.

"Toll receptor2", "TLR2" and "huTLR2" are used interchangeably, and refer to a human Toll receptor designated as "HuTLR2" by Rock *et al.*, Proc. Natl. Acad. Sci. USA 95, 588-593 (1998).

The term "expression vector" is used to define a vector, in which a nucleic acid encoding a PRO polypeptide herein is operably linked to control sequences capable of affecting its expression is a suitable host cells. Vectors ordinarily carry a replication site (although this is not necessary where chromosomal integration will occur). Expression vectors also include marker sequences which are capable of providing phenotypic selection in transformed cells. For example, E. coli is typically transformed using pBR322, a plasmid derived from an *E. coli* species (Bolivar, *et al.*, Gene 2: 95 [1977]). pBR322 contains genes for ampicillin and tetracycline resistance and thus provides easy means for identifying transformed cells, whether for purposes of cloning or expression. Expression vectors also optimally will contain sequences which are useful for the control of transcription and translation, e.g., promoters and Shine-Dalgarno sequences (for prokaryotes) or promoters and enhancers (for mammalian cells). The promoters may be, but need not be, inducible; even powerful constitutive promoters such as the CMV promoter for mammalian hosts have been found to produce the LHR without host cell toxicity. While it is conceivable that expression vectors need not contain any expression control, replicative sequences or selection genes, their absence may hamper the identification of hybrid

transformants and the achievement of high level hybrid immunoglobulin expression.

The term "lipopolysaccharide" or "LPS" is used herein as a synonym of "endotoxin." Lipopolysaccharides (LPS) are characteristic components of the outer membrane of Gram-negative bacteria, e.g., *Escherichia coli*. They consist of a polysaccharide part and a fat called lipid A. The polysaccharide, which varies from one bacterial species to another, is made up of the O-specific chain (built from repeating units of three to eight sugars) and the two-part core. Lipid A virtually always includes two glucosamine sugars modified by phosphate and a variable number of fatty acids. For further information see, for example, Rietschel and Brade, Scientific American August 1992, 54-61.

The term "septic shock" is used herein in the broadest sense, including all definitions disclosed in Bone, Ann. Intern Med. 114, 332-333 (1991). Specifically, septic shock starts with a systemic response to infection, a syndrome called sepsis. When this syndrome results in hypotension and organ dysfunction, it is called septic shock. Septic shock may be initiated by gram-positive organisms and fungi, as well as endotoxin-containing Gram-negative organisms. Accordingly, the present definition is not limited to "endotoxin shock."

The phrases "gene amplification" and "gene duplication" are used interchangeably and refer to a process by which multiple copies of a gene or gene fragment are formed in a particular cell or cell line. The duplicated region (a stretch of amplified DNA) is often referred to as "amplicon". Usually, the amount of the messenger RNA (mRNA) produced, i.e., the level of gene expression, also increases in the proportion of the number of copies made of the particular gene expressed.

"Tumor", as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues. The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia. More particular examples of such cancers include breast cancer, prostate cancer, colon cancer, squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, colorectal cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, vulval cancer, thyroid cancer, hepatic carcinoma and various types of head and neck cancer.

The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents the function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes (e.g. I131, I125, Y90 and Re186), chemotherapeutic agents, and toxins such as enzymatically active toxins of bacterial, fungal, plant or animal origin, or fragments thereof.

A "chemotherapeutic agent" is a chemical compound useful in the treatment of cancer. Examples of chemotherapeutic agents include adriamycin, doxorubicin, epirubicin, 5-fluorouracil, cytosine arabinoside ("Ara-C"), cyclophosphamide, thiotepa, busulfan, cytoxin, taxoids, e.g. paclitaxel (Taxol, Bristol-Myers Squibb Oncology, Princeton, NJ), and doxetaxel (Taxotere«, Rhone-Poulenc Rorer, Antony, France), toxotere, methotrexate, cisplatin, melphalan, vinblastine, bleomycin, etoposide, ifosfamide, mitomycin C, mitoxantrone, vincristine, vinorelbine, carboplatin, teniposide, daunomycin, carminomycin, aminopterin, dactinomycin,

mitomycins, esperamicins (see U.S. Pat. No. 4,675,187), melphalan and other related nitrogen mustards. Also included in this definition are hormonal agents that act to regulate or inhibit hormone action on tumors such as tamoxifen and onapristone.

A "growth inhibitory agent" when used herein refers to a compound or composition which inhibits growth of a cell, especially cancer cell overexpressing any of the genes identified herein, either in vitro or in vivo. Thus, the growth inhibitory agent is one which significantly reduces the percentage of cells overexpressing such genes in S phase. Examples of growth inhibitory agents include agents that block cell cycle progression (at a place other than S phase), such as agents that induce G1 arrest and M-phase arrest. Classical M-phase blockers include the vincas (vincristine and vinblastine), taxol, and topo II inhibitors such as doxorubicin, epirubicin, daunorubicin, etoposide, and bleomycin. Those agents that arrest G1 also spill over into S-phase arrest, for example, DNA alkylating agents such as tamoxifen, prednisone, dacarbazine, mechlorethamine, cisplatin, methotrexate, 5-fluorouracil, and ara-C. Further information can be found in The Molecular Basis of Cancer, Mendelsohn and Israel, eds., Chapter 1, entitled "Cell cycle regulation, oncogens, and antineoplastic drugs "by Murakami et al. (WB Saunders: Philadelphia, 1995), especially p.13.

"Doxorubicin" is an athracycline antibiotic.

The term "cytokine" is a generic term for proteins released by one cell population which act on another cell as intercellular mediators. Examples of such cytokines are lymphokines, monokines, and traditional polypeptide hormones. Included among the cytokines are growth hormone such as human growth hormone, N-methionyl human growth hormone, and bovine growth hormone; parathyroid hormone; thyroxine; insulin; proinsulin; relaxin; prorelaxin; and the like. As used herein, the term cytokine includes proteins from natural sources or from recombinant cell culture and biologically active equivalents of the native sequence cytokines.

"Immunological cross-reactivity" as used herein means that the candidate polypeptide is capable of competitively inhibiting the qualitative biological activity of a PRO213-1, PRO1330, or PRO1449 polypeptide having this activity with polyclonal antisera raised against the known active PRO213-1, PRO1330, or PRO1449 polypeptide. Such antisera may be prepared in conventional fashion by injecting goats or rabbits, for example, subcutaneously with the known active analogue in complete Freund's adjuvant, followed by booster intraperitoneal or subcutaneous injection in incomplete Freunds. The immunological cross-reactivity preferably is "specific", which means that the binding affinity of the immunological cross-reactive molecule (e.g., antibody) identified, to the corresponding PRO213-1, PRO1330, or PRO1449 polypeptide is significantly higher (preferably at least about 2-times, more preferably at least about 4-times, even more preferably at least about 6-times, most preferably at least about 8-times higher) than the binding affinity of that molecule to any other known native polypeptide.

"Native antibodies" and "native immunoglobulins" are usually heterotetrameric glycoproteins of about 150,000 daltons, composed of two identical light (L) chains and two identical heavy (H) chains. Each light chain is linked to a heavy chain by one covalent disulfide bond, while the number of disulfide linkages varies among the heavy chains of different immunoglobulin isotypes. Each heavy and light chain also has regularly spaced intrachain disulfide bridges. Each heavy chain has at one end a variable domain (VH) followed by a

number of constant domains. Each light chain has a variable domain at one end (VL) and a constant domain at its other end; the constant domain of the light chain is aligned with the first constant domain of the heavy chain, and the light chain variable domain is aligned with the variable domain of the heavy chain. Particular amino acid residues are believed to form an interface between the light- and heavy-chain variable domains.

The term "variable" refers to the fact that certain portions of the variable domains differ extensively in sequence among antibodies and are used in the binding and specificity of each particular antibody for its particular antigen. However, the variability is not evenly distributed throughout the variable domains of antibodies. It is concentrated in three segments called complementarity-determining regions (CDRs) or hypervariable regions both in the light-chain and the heavy-chain variable domains. The more highly conserved portions of variable domains are called the framework (FR). The variable domains of native heavy and light chains each comprise four FR regions, largely adopting a β-sheet configuration, connected by three CDRs, which form loops connecting, and in some cases forming part of, the β-sheet structure. The CDRs in each chain are held together in close proximity by the FR regions and, with the CDRs from the other chain, contribute to the formation of the antigen-binding site of antibodies (see Kabat et al., NIH Publ. No. 91-3242, Vol. I, pages 647-669 (1991)). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody-dependent cellular toxicity.

"Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')2, and Fv fragments; diabodies; linear antibodies (Zapata et al. , Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an F(ab')2 fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the VH-VL dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')2 antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

"Single-chain Fv" or "sFv" antibody fragments comprise the VH and VL domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the VH and VL domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenburg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (VH) connected to a light-chain variable domain (VL) in the same polypeptide chain (VH - VL). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labelled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes

a discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as the anti-ErbB2 antibodies disclosed herein and, optionally, a chemotherapeutic agent) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

II. Compositions and Methods of the Invention

1. Full-length PRO213 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO213. In particular, Applicants have identified and isolated cDNA encoding a PRO213 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that a portion of the PRO213 polypeptide has significant homology with the human growth arrest-specific 6 (gas6) protein. Accordingly, it is presently believed that PRO213 polypeptide disclosed in the present application may have the same or simular activity as does the gas6 protein.

2. Full-length PRO274 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO274. In particular, Applicants have identified and isolated cDNA encoding a PRO274 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO274 polypeptide have significant homology with the 7 transmembrane segment receptor proteins and Fn54 protein. Accordingly, it is presently believed that PRO274 polypeptide disclosed in the present application is a newly identified member of the 7 transmembrane segment receptor protein and/or Fn54 protein family.

3. Full-length PRO300 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO300. In particular, Applicants have identified and isolated cDNA encoding a PRO300 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO300 polypeptide have significant homology with the human Diff 33 protein. Accordingly, it is presently believed that PRO300 polypeptide disclosed in the present application is a newly identified member of the Diff 33 family.

4. Full-length PRO284 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO284. In particular, Applicants have identified and isolated cDNA encoding a PRO284 polypeptide, as disclosed in further detail in the Examples below. To Applicants present

knowledge, the UNQ247 (DNA23318-1211) nucleotide sequence encodes a novel factor; using BLAST and FastA sequence alignment computer programs, no sequence identities to any known proteins were revealed.

5. Full-length PRO296 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO296. In particular, Applicants have identified and isolated cDNA encoding a PRO296 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO296 polypeptide has significant similarity to the sarcoma-amplified SAS protein. Accordingly, it is presently believed that PRO296 polypeptide disclosed in the present application is a newly identified SAS protein homolog.

6. Full-length PRO329 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO329. In particular, Applicants have identified and isolated cDNA encoding a PRO329 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO329 polypeptide has significant similarity to a high affinity immunoglobulin F_c receptor. Accordingly, it is presently believed that PRO329 polypeptide disclosed in the present application is a newly identified F_c receptor homolog.

7. Full-length PRO362 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO362. In particular, Applicants have identified and isolated cDNA encoding a PRO362 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO362 polypeptide has significant similarity to the A33 antigen protein as well as the HCAR protein and the NrCAM related cell adhesion molecule. Accordingly, it is presently believed that PRO362 polypeptide disclosed in the present application is a newly A33 antigen and HCAR protein homolog.

8. Full-length PRO363 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO363. In particular, Applicants have identified and isolated cDNA encoding a PRO363 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO363 polypeptide has significant similarity to the cell surface protein HCAR. Accordingly, it is presently believed that PRO363 polypeptide disclosed in the present application is a newly HCAR homolog.

9. **Full-length PRO868 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO868. In particular, Applicants have identified and isolated cDNA encoding a PRO868 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO868 polypeptide has significant similarity to the tumor necrosis factor receptor. Accordingly, it is presently believed that PRO868 polypeptide disclosed in the present application is a newly identified member of the tumor necrosis factor receptor family of proteins.

10. **Full-length PRO382 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO382. In particular, Applicants have identified and isolated cDNA encoding a PRO382 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the native PRO382 polypeptide shares significant homology with various serine protease proteins. Applicants have also found that the DNA encoding the PRO382 polypeptide shares significant homology with nucleic acid encoding various serine protease proteins. Accordingly, it is presently believed that PRO382 polypeptide disclosed in the present application is a newly identified serine protease homolog.

11. **Full-length PRO545 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO545. In particular, Applicants have identified and isolated cDNA encoding a PRO545 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO545 polypeptide have significant homology with the sequences identified designated as; human metalloproteinase ("P_W01825"), mouse meltrin alpha ("S60257"), metalloprotease-disintegrin meltrin-alpha ("GEN13695"), ADAM 13 - *Xenopus laevis* ("XLU66003_1"), mouse meltrin beta ("S60258"), rabbit metalloprotease-disintegrin meltrin-beta, ("GEN13696"), human meltrin S ("AF023477_1"), human meltrin precursor ("AF023476_1"), human ADAM 21 ("AF029900_1"), and human ADAM 20 ("AF029899_1"), thereby indicating that PRO545 may be a novel meltrin protein. Accordingly, it is presently believed that the PRO545 polypeptide disclosed in the present application is a newly identified member of the meltrin family and possesses the cellular adhesiveness typical of the meltrin proteins which comprise both metalloprotease and disintegrin domains.

12. **Full-length PRO617 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO617. In particular, Applicants have identified and isolated cDNA encoding a PRO617 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO617 polypeptide shares significant

homology with the CD24 protein. Applicants have also found that the DNA encoding the PRO617 polypeptide has significant homology with DNA encoding the CD24 protein. Accordingly, it is presently believed that PRO617 polypeptide disclosed in the present application is a newly identified CD24 homolog.

13. **Full-length PRO700 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO700. In particular, Applicants have identified and isolated cDNA encoding a PRO700 polypeptide, as disclosed in further detail in the Examples below. Analysis of the amino acid sequence of the full-length PRO700 polypeptide using BLAST and FastA sequence alignment computer programs, suggests that various portions of the PRO700 polypeptide possess significant sequence similarity to various protein disulfide isomerases. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant sequence similarity between the PRO700 amino acid sequence and the following Dayhoff sequences; polypeptide with protein disulfide isomerase activity, designated as ("P_P80664"), human PDI, designated as ("P_R51696"), human PDI, designated as (P_R25297"), probable protein disulfide isomerase er-60 precursor, designated as ("ER60_SCHMA"), protein disulfide isomerase precursor - *Drosophila melanogaster*, designated as ("PDI_DROME"), protein disulfide-isomerase precursor - *Nicotiana tabaccum*, designated as ("NTPDIGENE_1"), protein disulfide isomerase - *Onchocerca volvulus*, designated as ("OVU12440_1"), human probable protein disulfide isomerase p5 precursor , designated as ("ERP5_HUMAN"), human protein disulfide isomerase-related protein 5, ("HSU79278_1 "), and protein disulfide isomerase precursor / prolyl 4- hydroxy, ("PDI_HUMAN"), thereby indicating that PRO700 may be a novel protein disulfide isomerase. Accordingly, it is presently believed that PRO700 polypeptide disclosed in the present application is a newly identified member of the protein disulfide isomerase family and possesses the ability to catalyze the formation of disulfide bonds typical of the protein disulfide isomerase family.

14. **Full-length PRO702 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO702. In particular, Applicants have identified and isolated cDNA encoding a PRO702 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO702 polypeptide has significant similarity to the conglutinin protein. Accordingly, it is presently believed that PRO702 polypeptide disclosed in the present application is a newly identified conglutinin homolog.

15. **Full-length PRO703 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO703. In particular, Applicants have identified and isolated cDNA encoding a PRO703 polypeptide, as disclosed in further detail in the Examples below. Analysis of the amino acid sequence of the full-length PRO703 polypeptide using BLAST and FastA sequence alignment computer

programs, suggests that various portions of the PRO703 polypeptide possess significant sequence similarity to the VLCAS protein, thereby indicating that PRO703 may be a novel VLCAS protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant sequence similarity between the PRO703 amino acid sequence and the following Dayhoff sequences, human mRNA for very-long-chain acyl-CoA, ("D88308"), rat mRNA for very-long-chain acyl-CoA synthetase, ("D85100"), *Mus musculus* fatty acid transport protein, ("MMU15976"), human very-long-chain acyl-CoA synthetase, ("D88308_1"), *Mus musculus* very-long-chain acyl-CoA synthetase, ("AF033031_1"), very-long-chain acyl-CoA synthetase - *Rattus*, ("D85100_1"), rat long-chain fatty acid transport protein, ("FATP_RAT"), mouse long-chain fatty acid transport protein, ("FATP_MOUSE"), probable long-chain fatty acid transport protein, ("FAT1_YEAST"), and fatty acid transporter protein, ("CHY15839_2"), thereby indicating that PRO703 may be a novel VLCAS. Accordingly, it is presently believed that PRO703 polypeptide disclosed in the present application is a newly identified member of the VLCAS family and possesses the ability to facilitate the cellular transport of long and very long chain fatty acids typical of the VLCAS family.

16. **<u>Full-length PRO705 Polypeptides</u>**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO705. In particular, Applicants have identified and isolated cDNA encoding a PRO705 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO705 polypeptide has significant similarity to the K-glypican protein. Accordingly, it is presently believed that PRO705 polypeptide disclosed in the present application is a newly identified member of the glypican family of proteoglycan proteins.

17. **<u>Full-length PRO708 Polypeptides</u>**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO708. In particular, Applicants have identified and isolated cDNA encoding a PRO708 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO708 polypeptide has significant homology with the aryl sulfatase proteins. Applicants have also found that the DNA encoding the PRO708 polypeptide has significant homology with DNA encoding the aryl sulfatase proteins. Accordingly, it is presently believed that PRO708 polypeptide disclosed in the present application is a newly identified aryl sulfatase homolog.

18. **<u>Full-length PRO320 Polypeptides</u>**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO320. In particular, Applicants have identified and isolated cDNA encoding a PRO320 polypeptide, as disclosed in further detail in the Examples below. Analysis of the amino acid sequence of the full-length PRO320 polypeptide using BLAST and FastA sequence alignment computer programs, suggests that various portions of the PRO320 polypeptide have significant homology to the fibulin

protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO320 amino acid sequence and the following Dayhoff sequences, human fibulin-2 precursor, designated "FBL2_HUMAN", human fibulin-1 isoform a precursor, designated "FBLA_HUMAN", ZK783.1 - Caenorhabditis elegans, designated "CELZK783_1", human-notch2, designated "HSU77493_1", Nel protein precursor - rattus norvegicus, designated "NEL_RAT", Mus musculus cell surface protein, designated "D32210_1", mouse (fragment) Notch B protein, designated "A49175", C50H2.3a - Caenorhabditis elegans, designated "CEC50H2_3", MEC-9L - Caenorhabditis elegans, designated "CEU33933_1", and Mus musculus notch 4, designated "10 MMMHC29N7_2", thereby indicating that PRO320 may be a novel fibulin or fibulin-like protein. Accordingly, it is presently believed that PRO320 polypeptide disclosed in the present application is a newly identified member of the fibulin family and possesses biological activity typical of the fibulin family.

19. Full-length PRO324 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO324. In particular, Applicants have identified and isolated cDNA encoding a PRO324 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO324 polypeptide has significant similarity to oxidoreductases. Accordingly, it is presently believed that PRO324 polypeptide disclosed in the present application is a newly identified oxidoreductase homolog.

20. Full-length PRO351 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO351. In particular, Applicants have identified and isolated cDNA encoding a PRO351 polypeptide, as disclosed in further detail in the Examples below. Analysis of the amino acid sequence of the full-length PRO351 polypeptide using BLAST and FastA sequence alignment computer programs, suggests that various portions of the PRO351 polypeptide possess significant sequence similarity to the prostasin protein, thereby indicating that PRO351 may be a novel prostasin protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant sequence similarity between the PRO351 amino acid sequence and the following Dayhoff sequences, "AC003965_1", "CELC07G1_7", "GEN12917", "HEPS_HUMAN", "GEN14584", "MCT6_MOUSE", "HSU75329_1", "PLMN_ERIEU", "TRYB_HUMAN", and "P_W22987". Accordingly, it is presently believed that PRO351 polypeptide disclosed in the present application is a newly identified member of the prostasin family and possesses properties and activities typical of the prostasin family.

21. Full-length PRO352 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO352. In particular, Applicants have identified and isolated cDNA

encoding a PRO352 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO352 polypeptide has significant similarity to the butyrophilin protein. Accordingly, it is presently believed that PRO352 polypeptide disclosed in the present application is a newly identified butyrophilin homolog.

22. **Full-length PRO381 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO381. In particular, Applicants have identified and isolated cDNA encoding a PRO381 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO381 polypeptide has significant similarity to immunophilin proteins. Accordingly, it is presently believed that PRO381 polypeptide disclosed in the present application is a newly identified FKBP immunophilin homolog.

23. **Full-length PRO386 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO386. In particular, Applicants have identified and isolated cDNA encoding a PRO386 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO386 polypeptide has significant similarity to the beta-2 subunit of a sodium channel protein. Accordingly, it is presently believed that PRO386 polypeptide disclosed in the present application is homolog of a beta-2 subunit of a sodium channel expressed in mammalian cells.

24. **Full-length PRO540 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO540. In particular, Applicants have identified and isolated cDNA encoding a PRO540 polypeptide, as disclosed in further detail in the Examples below. Analysis of the amino acid sequence of the full-length PRO540 polypeptide using BLAST and FastA sequence alignment computer programs, suggests that various portions of the PRO540 polypeptide possess significant sequence similarity to the LCAT protein, thereby indicating that PRO540 may be a novel LCAT protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant sequence similarity between the PRO540 amino acid sequence and the following Dayhoff sequences, phosphatidylcholine-sterol acyltransferase, designated "LCAT_HUMAN", hypothetical 75.4 kd protein, designated "YN84_YEAST", *Bacillus licheniformis* esterase, designated "BLU35855_1", macrotetrolide resistance protein - *Streptomyces*, designated "JH0655", T-cell receptor delta chain precursor, designated "C30583", Rhesus kringle 2, designated "P_W07551", RAGE-1 ORF5, designated "HSU46191_3", human Ig kappa chain VKIII-JK3, designated "HSU07466_1", and *Alstroemeria inodora* reverse transcriptase, designated "ALI223606_1". Accordingly, it is presently believed that PRO540 polypeptide disclosed in the present application is a newly identified member

of the LCAT protein family and possesses lipid transport capability typical of the LCAT family.

25. Full-length PRO615 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO615. In particular, Applicants have identified and isolated cDNA encoding a PRO615 polypeptide, as disclosed in further detail in the Examples below. Analysis of the amino acid sequence of the full-length PRO615 polypeptide using BLAST and FastA sequence alignment computer programs, suggests that various portions of the PRO615 polypeptide possess significant sequence similarity to the human synaptogyrin protein, thereby indicating that PRO615 may be a novel synaptogyrin protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant sequence similarity between the PRO615 amino acid sequence and the following Dayhoff sequences, "AF039085_1", "RNU39549_1", "CELT08A9_8", "FSU62028_1", "S73645", "Y348_MYCPN", "AC000103_5", "", "RT12_LEITA", and "EBVLMP218_1". Accordingly, it is presently believed that PRO615 polypeptide disclosed in the present application is a newly identified member of the synaptogyrin family and possesses activity and properties typical of the synaptogyrin family.

26. Full-length PRO618 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO618. In particular, Applicants have identified and isolated cDNA encoding a PRO618 polypeptide, as disclosed in further detail in the Examples below. Analysis of the amino acid sequence of the full-length PRO618 polypeptide using BLAST and FastA sequence alignment computer programs, suggests that various portions of the PRO618 polypeptide possess significant sequence similarity to the enteropeptidase protein, thereby indicating that PRO618 may be a novel enteropeptidase. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant sequence similarity between the PRO618 amino acid sequence and the following Dayhoff sequences, "P_W22987", "KAL_HUMAN", "AC003965_1", "GEN12917", "ENTK_HUMAN", "FA11_HUMAN", "HSU75329_1", "P_W22986", and "PLMN_HORSE". Accordingly, it is presently believed that PRO618 polypeptide disclosed in the present application is a newly identified member of the enteropeptidase family and possesses catalytic activity typical of the enteropeptidase family.

27. Full-length PRO719 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO719. In particular, Applicants have identified and isolated cDNA encoding a PRO719 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO719 polypeptide has significant similarity to the lipoprotein lipase H protein. Accordingly, it is presently believed that PRO719 polypeptide disclosed in the present application is a newly identified lipoprotein lipase H homolog.

28. Full-length PRO724 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO724. In particular, Applicants have identified and isolated cDNA encoding a PRO724 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO724 polypeptide has significant similarity to the human low density lipoprotein (LDL) receptor protein. Accordingly, it is presently believed that PRO724 polypeptide disclosed in the present application is a newly identified LDL receptor homolog.

29. Full-length PRO772 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO772. In particular, Applicants have identified and isolated cDNA encoding a PRO772 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO772 polypeptide has significant similarity to the human A4 protein. Accordingly, it is presently believed that PRO772 polypeptide disclosed in the present application is a newly identified A4 protein homolog.

30. Full-length PRO852 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO852. In particular, Applicants have identified and isolated cDNA encoding a PRO852 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO852 polypeptide has significant similarity to various protease proteins. Accordingly, it is presently believed that PRO852 polypeptide disclosed in the present application is a newly identified protease enzyme homolog.

31. Full-length PRO853 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO853. In particular, Applicants have identified and isolated cDNA encoding a PRO853 polypeptide, as disclosed in further detail in the Examples below. Analysis of the amino acid sequence of the full-length PRO853 polypeptide using BLAST and FastA sequence alignment computer programs, suggests that various portions of the PRO853 polypeptide possess significant sequence similarity to the reductase protein, thereby indicating that PRO853 may be a novel reductase. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant sequence similarity between the PRO853 amino acid sequence and the following Dayhoff sequences, "P_W03198", "CEC15H11_6", "MTV030_12", "P_W15759", "S42651", "ATAC00234314", "MTV022_13", "SCU43704_1", "CELE04F6_7", and "ALFA_1". Accordingly, it is presently believed that PRO853 polypeptide disclosed in the present application is a newly identified member of the reductase family and possesses the antioxidant enzymatic activity typical of the reductase family.

32. **Full-length PRO860 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO860. In particular, Applicants have identified and isolated cDNA encoding a PRO860 polypeptide, as disclosed in further detail in the Examples below. Analysis of the amino acid sequence of the full-length PRO860 polypeptide using BLAST and FastA sequence alignment computer programs, suggests that various portions of the PRO860 polypeptide possess significant sequence similarity to the neurofascin protein, thereby indicating that PRO860 may be a novel neurofascin. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant sequence similarity between the PRO860 amino acid sequence and the following Dayhoff sequences, "AF040990_1", "AF041053_1", "CELZK377_2", "RNU81035_1", "D86983_1", "S26180", "MMBIG2A_1", "S46216", and "RNU68726_1". Accordingly, it is presently believed that PRO860 polypeptide disclosed in the present application is a newly identified member of the neurofascin family and possesses the cellular adhesion properties typical of the neurofascin family.

33. **Full-length PRO846 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO846. In particular, Applicants have identified and isolated cDNA encoding a PRO846 polypeptide, as disclosed in further detail in the Examples below. Analysis of the amino acid sequence of the full-length PRO846 polypeptide using BLAST and FastA sequence alignment computer programs, suggests that various portions of the PRO846 polypeptide possess significant sequence similarity to the CMRF35 protein, thereby indicating that PRO846 may be a novel CMRF35 protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant sequence similarity between the PRO846 amino acid sequence and the following Dayhoff sequences, "CM35_HUMAN", "AF035963_1", "PIGR_RABIT", "AF043724_1", "RNU89744_1", "A52091_1", "S48841", "ELK06A9_3", and "AF049588_1". Accordingly, it is presently believed that PRO846 polypeptide disclosed in the present application is a newly identified member of the CMRF35 protein family and possesses properties typical of the CMRF35 protein family.

34. **Full-length PRO862 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO862. In particular, Applicants have identified and isolated cDNA encoding a PRO862 polypeptide, as disclosed in further detail in the Examples below. Analysis of the amino acid sequence of the full-length PRO862 polypeptide using BLAST and FastA sequence alignment computer programs, suggests that various portions of the PRO862 polypeptide possess significant sequence similarity to the lysozyme protein, thereby indicating that PRO862 may be a novel lysozyme protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant sequence similarity between the PRO862 amino acid sequence and the following Dayhoff sequences, "P_P90343", and "LYC_HUMAN.

Accordingly, it is presently believed that PRO862 polypeptide disclosed in the present application is a newly identified member of the lysozyme family and possesses catalytic activity typical of the lysozyme family.

35. Full-length PRO864 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO864. In particular, Applicants have identified and isolated cDNA encoding a PRO864 polypeptide, as disclosed in further detail in the Examples below. Analysis of the amino acid sequence of the full-length PRO864 polypeptide using BLAST and FastA sequence alignment computer programs, suggests that various portions of the PRO864 polypeptide possess significant sequence similarity to the Wnt-4 protein, thereby indicating that PRO864 may be a novel Wnt-4 protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant sequence similarity between the PRO864 amino acid sequence and the following Dayhoff sequences, "WNT4_MOUSE", "WNT3_MOUSE", "WN5A_HUMAN", "WN7B_MOUSE", "WN3A_MOUSE", "XLU66288_1", "WN13_HUMAN", "WN5B_ORYLA", "WNT2_MOUSE", and "WN7A_MOUSE". Accordingly, it is presently believed that PRO864 polypeptide disclosed in the present application is a newly identified member of the Wnt-4 protein family and possesses properties typical of the Wnt-4 protein family.

36. Full-length PRO792 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO792. In particular, Applicants have identified and isolated cDNA encoding a PRO792 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO792 polypeptide has significant similarity to the CD23 protein. Accordingly, it is presently believed that PRO792 polypeptide disclosed in the present application is a newly identified CD23 homolog.

37. Full-length PRO866 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO866. In particular, Applicants have identified and isolated cDNA encoding a PRO866 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO866 polypeptide has significant similarity to various mindin and spondin proteins. Accordingly, it is presently believed that PRO866 polypeptide disclosed in the present application is a newly identified mindin/spondin homolog.

38. Full-length PRO871 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO871. In particular, Applicants have identified and isolated cDNA encoding a PRO871 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA

sequence alignment computer programs, Applicants found that the PRO871 polypeptide has significant similarity to the CyP-60 protein. Accordingly, it is presently believed that PRO871 polypeptide disclosed in the present application is a newly identified member of the cyclophilin protein family and possesses activity typical of the cyclophilin protein family.

39. **Full-length PRO873 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO873. In particular, Applicants have identified and isolated cDNA encoding a PRO873 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO873 polypeptide has significant similarity to a human liver carboxylesterase. Accordingly, it is presently believed that PRO873 polypeptide disclosed in the present application is a newly identified member of the carboxylesterase family and possesses enzymatic activity typical of the carboxylesterase family.

40. **Full-length PRO940 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO940. In particular, Applicants have identified and isolated cDNA encoding a PRO940 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO940 polypeptide has significant similarity to CD33 and the OB binding protein-2. Accordingly, it is presently believed that PRO940 polypeptide disclosed in the present application is a newly CD33 and/or OB binding protein-2 homolog.

41. **Full-length PRO941 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO941. In particular, Applicants have identified and isolated cDNA encoding a PRO941 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO941 polypeptide has significant similarity to one or more cadherin proteins. Accordingly, it is presently believed that PRO941 polypeptide disclosed in the present application is a newly identified cadherin homolog.

42. **Full-length PRO944 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO944. In particular, Applicants have identified and isolated cDNA encoding a PRO944 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO944 polypeptide has significant similarity to the CPE-R cell surface protein. Accordingly, it is presently believed that PRO944 polypeptide disclosed in the present application is a newly identified CPE-R homolog.

43. Full-length PRO983 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO983. In particular, Applicants have identified and isolated cDNA encoding a PRO983 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO983 polypeptide has significant similarity to the vesicle-associated protein, VAP-33. Accordingly, it is presently believed that PRO983 polypeptide disclosed in the present application is a newly identified member of the vesicle-associated membrane protein family and possesses activity typical of vesicle-associated membrane proteins.

44. Full-length PRO1057 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO1057. In particular, Applicants have identified and isolated cDNA encoding a PRO1057 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO1057 polypeptide has significant similarity to various protease proteins. Accordingly, it is presently believed that PRO1057 polypeptide disclosed in the present application is a newly identified protease homolog.

45. Full-length PRO1071 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO1071. In particular, Applicants have identified and isolated cDNA encoding a PRO1071 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO1071 polypeptide has significant similarity to the thrombospondin protein. Accordingly, it is presently believed that PRO1071 polypeptide disclosed in the present application is a newly identified thrombospondin homolog.

46. Full-length PRO1072 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO1072. In particular, Applicants have identified and isolated cDNA encoding a PRO1072 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO1072 polypeptide has significant similarity to various reductase proteins. Accordingly, it is presently believed that PRO1072 polypeptide disclosed in the present application is a newly identified member of the reductase protein family.

47. Full-length PRO1075 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO1075. In particular, Applicants have identified and isolated cDNA encoding a PRO1075 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and

FastA sequence alignment computer programs, Applicants found that the PRO1075 polypeptide has significant similarity to protein disulfide isomerase. Accordingly, it is presently believed that PRO1075 polypeptide disclosed in the present application is a newly identified member of the protein disulfide isomerase family and possesses activity typical of that family.

48. Full-length PRO181 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO181. In particular, Applicants have identified and isolated cDNA encoding a PRO181 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO181 polypeptide has significant similarity to the cornichon protein. Accordingly, it is presently believed that PRO181 polypeptide disclosed in the present application is a newly identified cornichon homolog.

49. Full-length PRO195 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO195. In particular, Applicants have identified and isolated cDNA encoding a PRO195 polypeptide, as disclosed in further detail in the Examples below. The PRO195-encoding clone was isolated from a human fetal placenta library using a trapping technique which selects for nucleotide sequences encoding secreted proteins. To Applicants present knowledge, the UNQ169 (DNA26847-1395) nucleotide sequence encodes a novel factor; using BLAST and FastA sequence alignment computer programs, no sequence identities to any known proteins were revealed.

50. Full-length PRO865 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO865. In particular, Applicants have identified and isolated cDNA encoding a PRO865 polypeptide, as disclosed in further detail in the Examples below. The PRO865-encoding clone was isolated from a human fetal kidney library using a trapping technique which selects for nucleotide sequences encoding secreted proteins. Thus, the PRO865-encoding clone may encode a secreted factor. To Applicants present knowledge, the UNQ434 (DNA53974-1401) nucleotide sequence encodes a novel factor; using BLAST and FastA sequence alignment computer programs, no sequence identities to any known proteins were revealed.

51. Full-length PRO827 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO827. In particular, Applicants have identified and isolated cDNA encoding a PRO827 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO827 polypeptide has significant similarity

to VLA-2 and various other integrin proteins. Accordingly, it is presently believed that PRO827 polypeptide disclosed in the present application is a novel integrin protein or splice variant thereof.

52. **Full-length PRO1114 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO1114. In particular, Applicants have identified and isolated cDNA encoding a PRO1114 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO1114 polypeptide has significant similarity to the cytokine receptor family of proteins. Accordingly, it is presently believed that PRO1114 polypeptide disclosed in the present application is a newly identified member of the cytokine receptor family of proteins and possesses activity typical of that family.

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO1114 interferon receptor (UNQ557). In particular, cDNA encoding a PRO1114 interferon receptor polypeptide has been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by DNA57033-1403 as well as all further native homologues and variants included in the foregoing definition of PRO1114 interferon receptor, will be referred to as "PRO1114 interferon receptor", regardless of their origin or mode of preparation.

Using the WU-BLAST2 sequence alignment computer program, it has been found that a full-length native sequence PRO1114 interferon receptor polypeptide (shown in Figure 142 and SEQ ID NO:352) has sequence identity with the other known interferon receptors. Accordingly, it is presently believed that PRO1114 interferon receptor possesses activity typical of other interferon receptors.

53. **Full-length PRO237 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO237. In particular, Applicants have identified and isolated cDNA encoding a PRO237 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO237 polypeptide has significant similarity to carbonic anhydrase. Accordingly, it is presently believed that PRO237 polypeptide disclosed in the present application is a newly identified carbonic anhydrase homolog.

54. **Full-length PRO541 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO541. In particular, Applicants have identified and isolated cDNA encoding a PRO541 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO541 polypeptide has significant similarity

to a trypsin inhibitor protein. Accordingly, it is presently believed that PRO541 polypeptide disclosed in the present application is a newly identified member of the trypsin inhibitor protein family.

55. Full-length PRO273 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO273. In particular, Applicants have identified and isolated cDNA encoding a PRO273 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO273 polypeptide have significant sequence identity with various chemokines. Accordingly, it is presently believed that PRO273 polypeptide disclosed in the present application is a newly identified member of the chemokine family and possesses activity typical of the chemokine family.

56. Full-length PRO701 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO701. In particular, Applicants have identified and isolated cDNA encoding a PRO701 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO701 polypeptide have significant homology with the neuroligins 1, 2 and 3 and esterases including carboxyesterases and acytlcholinesterases. Accordingly, it is presently believed that PRO701 polypeptide disclosed in the present application is a newly identified member of the neuroligin family and is involved in mediating recognition processes between neurons and/or functions as a cell adhesin molecule as is typical of neuroligins.

57. Full-length PRO704 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO704. In particular, Applicants have identified and isolated cDNA encoding a PRO704 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO704 polypeptide have significant homology with the VIP36 and GP36b. Accordingly, it is presently believed that PRO704 polypeptide disclosed in the present application is a newly identified member of the vesicular integral membrane protein family and possesses the ability to bind to sugars and cycle between the plasma membrane and the Golgi typical of this family.

58. Full-length PRO706 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO706. In particular, Applicants have identified and isolated cDNA encoding a PRO706 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO706 polypeptide have

sequence identity with the human prostatic acid phosphatase precursor and the human lysosomal acid phosphatase precursor. Accordingly, it is presently believed that PRO706 polypeptide disclosed in the present application is a newly identified member of the human prostatic acid phosphatase precursor family and possesses phosphatase typical of the acid phosphatase family.

59. Full-length PRO707 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO707. In particular, Applicants have identified and isolated cDNA encoding a PRO707 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO707 polypeptide have significant homology with cadherins, particularly cadherin FIB3 found in fibroblasts. Accordingly, it is presently believed that PRO707 polypeptide disclosed in the present application is a newly identified member of the cadherin family and possesses cell interaction signaling typical of the cadherin family.

60. Full-length PRO322 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO322. In particular, Applicants have identified and isolated cDNA encoding a PRO322 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO322 polypeptide have significant homology with human neuropsin, serine protease, neurosin and trypsinogen. Accordingly, it is presently believed that PRO322 polypeptide disclosed in the present application is a newly identified member of the serine protease family and possesses protease activity typical of this family. It is also believed that PRO322 is involved in hippocampal plasticity and is associated with extracellular matrix modifications and cell migrations.

61. Full-length PRO526 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO526. In particular, Applicants have identified and isolated cDNA encoding a PRO526 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO526 polypeptide have significant homology with the acid labile subunit of the insulin-like growth factor complex (ALS), as well carboxypeptidase, SLIT, and platelet glycoprotein V. Accordingly, it is presently believed that PRO526 polypeptide disclosed in the present application is a newly identified member of the leucine-repeat rich superfamily, and possesses protein-protein interaction capabilities typical of this family.

62. Full-length PRO531 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides

referred to in the present application as PRO531. In particular, Applicants have identified and isolated cDNA encoding a PRO531 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO531 polypeptide have significant sequence identity and similarity with members of the cadherin superfamily, particularly, protocadherin 3. Accordingly, it is presently believed that PRO531 polypeptide disclosed in the present application is a newly identified member of the cadherin superfamily, and is a protocadherin. PRO531 is a transmembrane protein which has extracellular cadherin motifs. PRO531 is believed to be involved in cell-cell activity, in particular, cell signaling.

63. Full-length PRO534 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO534. In particular, Applicants have identified and isolated cDNA encoding a PRO534 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO534 polypeptide have significant identity or similarity with the putative disulfide isomerase erp38 precursor and thioredoxin c-3. Accordingly, it is presently believed that PRO534 polypeptide disclosed in the present application is a newly identified member of the disulfide isomerase family and possesses the ability to recognize and unscramble either intermediate or incorrect folding patterns typical of this family.

64. Full-length PRO697 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO697. In particular, Applicants have identified and isolated cDNA encoding a PRO697 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO697 polypeptide have significant identity or similarity with sFRP-2, sFRP-1 and SARP-1, -2 and -3. Accordingly, it is presently believed that PRO697 polypeptide disclosed in the present application is a newly identified member of the sFRP family and possesses activity related to the Wnt signal pathway.

65. Full-length PRO717 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO717. In particular, Applicants have identified and isolated cDNA encoding a PRO717 polypeptide, as disclosed in further detail in the Examples below. To Applicants present knowledge, the UNQ385 (DNA50988-1326) nucleotide sequence encodes a novel factor; using BLAST and FastA sequence alignment computer programs, no significant sequence identities to any known human proteins were revealed.

66. Full-length PRO731 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides

referred to in the present application as PRO731. In particular, Applicants have identified and isolated cDNA encoding a PRO731 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO731 polypeptide have significant homology with the protocadherins 4, 68, 43, 42, 3, and 5. Accordingly, it is presently believed that PRO731 polypeptide disclosed in the present application is a newly identified member of the protocadherin family and possesses cell-cell aggregation or signaling activity or signal transduction involvement typical of this family.

67. **Full-length PRO218 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO218. In particular, Applicants have identified and isolated cDNA encoding a PRO218 polypeptide, as disclosed in further detail in the Examples below. The PRO218-encoding clone was isolated from a human fetal kidney library. To Applicants present knowledge, the UNQ192 (DNA30867-1335) nucleotide sequence encodes a novel factor; using BLAST and FastA sequence alignment computer programs, no significant sequence identities to any known proteins were revealed. Some sequence identity was found with membrane regulator proteins, indicating that PRO218 may function as a membrane regulator.

68. **Full-length PRO768 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO768. In particular, Applicants have identified and isolated cDNA encoding a PRO768 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO768 polypeptide have significant homology with integrins, including integrin 7 and 6. Accordingly, it is presently believed that PRO768 polypeptide disclosed in the present application is a newly identified member of the integrin family, either a homologue or a splice variant of integrin 7, and is involved with cell adhesion and communication between muscle cells and the extracellular matrix.

69. **Full-length PRO771 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO771. In particular, Applicants have identified and isolated cDNA encoding a PRO771 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO771 polypeptide have significant sequence identity and similarity with testican. Accordingly, it is presently believed that PRO771 polypeptide disclosed in the present application is a newly identified member of the testican family and possesses cell signaling, binding, or adhesion properties, typical of this family.

70. **Full-length PRO733 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO733. In particular, Applicants have identified and isolated cDNA encoding a PRO733 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO733 polypeptide have significant sequence identity with the T1/ST receptor binding protein. Accordingly, it is presently believed that PRO733 polypeptide disclosed in the present application is a newly identified member of the interleukin-like family binding proteins which may be a cytokine and which may be involved in cell signaling. It is believed that PRO733 is an ApoAIV homologue.

71. **Full-length PRO162 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO162. In particular, Applicants have identified and isolated cDNA encoding a PRO162 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO162 polypeptide have significant homology with human pancreatitis-associated protein (PAP). Applicants have also found that the DNA encoding the PRO162 polypeptide has significant homology with bovine lithostathine precursor and bovine pancreatic thread protein (PTP). Accordingly, it is presently believed that PRO162 polypeptide disclosed in the present application is a newly identified member of the pancreatitis-associated protein family and possesses activity typical of the pancreatitis-associated protein family.

72. **Full-length PRO788 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO788. In particular, Applicants have identified and isolated cDNA encoding a PRO788 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO788 polypeptide have significant homology with the anti-neoplastic urinary protein. Applicants have also found that the DNA encoding the PRO788 polypeptide has significant homology with human E48 antigen, human component B protein, and human prostate stem cell antigen. Accordingly, it is presently believed that PRO788 polypeptide disclosed in the present application is a newly identified member of the anti-neoplastic urinary protein family and possesses anti-neoplastic activity typical of the anti-neoplastic urinary protein family.

73. **Full-length PRO1008 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO1008. In particular, Applicants have identified and isolated cDNA encoding a PRO1008 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO1008

polypeptide have significant sequence identity and similarity with mouse dkk-1 (mdkk-1). Accordingly, it is presently believed that PRO1008 polypeptide disclosed in the present application is a newly identified member of the dkk-1 family and possesses head inducing activity typical of this family.

74. **Full-length PRO1012 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO1012. In particular, Applicants have identified and isolated cDNA encoding a PRO1012 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO1012 polypeptide have sequence identity with disulfide isomerase. Accordingly, it is presently believed that PRO1012 polypeptide disclosed in the present application is a newly identified member of the ER retained protein family and possesses activity related to the processing, production and/or folding of polypeptides typical of the disulfide isomerase family.

75. **Full-length PRO1014 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO1014. In particular, Applicants have identified and isolated cDNA encoding a PRO1014 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO1014 polypeptide have sequence identity with reductase and dehydrogenase. Accordingly, it is presently believed that PRO1014 polypeptide disclosed in the present application is a newly identified member of the reductase super family and possesses reduction capabilities typical of this family.

76. **Full-length PRO1017 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO1017. In particular, Applicants have identified and isolated cDNA encoding a PRO1017 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO1017 polypeptide have sequence identity with HNK-1 sulfotransferase. Accordingly, it is presently believed that PRO1017 polypeptide disclosed in the present application is a newly identified member of the HNK-1 sulfotransferase family and is involved with the synthesis of HNK-1 carbohydrate epitopes typical of this family.

77. **Full-length PRO474 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO474. In particular, Applicants have identified and isolated cDNA encoding a PRO474 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO474 polypeptide have

sequence identity with dehydrogenase, glucose dehydrogenase and oxidoreductase. Accordingly, it is presently believed that PRO474 polypeptide disclosed in the present application is a newly identified member of the dehydrogenase family and is involved in the oxidation of glucose.

78. Full-length PRO1031 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO1031. In particular, Applicants have identified and isolated cDNA encoding a PRO1031 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO1031 polypeptide have sequence identity with IL-17 and CTLA-8. Accordingly, it is presently believed that PRO1031 polypeptide disclosed in the present application is a newly identified member of the cytokine family and thus may be involved in inflammation and/or the immune system.

79. Full-length PRO938 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO938. In particular, Applicants have identified and isolated cDNA encoding a PRO938 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO938 polypeptide has significant similarity to protein disulfide isomerase. Accordingly, it is presently believed that PRO938 polypeptide disclosed in the present application is a newly identified member of the thioredoxin family proteins and possesses activity typical of protein disulfide isomerase.

80. Full-length PRO1082 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO1082. In particular, Applicants have identified and isolated cDNA encoding a PRO1082 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO1082 polypeptide have sequence identity with a lectin-like oxidized LDL receptor appearing in the database as "AB010710_1". Accordingly, it is presently believed that PRO1082 polypeptide disclosed in the present application is a newly identified member of the LDL receptor family.

81. Full-length PRO1083 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO1083. In particular, Applicants have identified and isolated cDNA encoding a PRO1083 polypeptide, as disclosed in further detail in the Examples below. The PRO1083-encoding clone was isolated from a human fetal kidney library using a trapping technique which selects for nucleotide sequences encoding secreted proteins. To Applicants present knowledge, the UNQ540 (DNA50921-1458)

nucleotide sequence encodes a novel factor; using BLAST and FastA sequence alignment computer programs, some sequence identity with a 7TM receptor, latrophilin related protein 1 and a macrophage restricted cell surface glycoprotein was shown. The kinase phosphorylation site and G-coupled receptor domain shown in Figure 204 indicate that PRO1083 is a novel member of the 7TM receptor superfamily.

82. **Full-length PRO200 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as VEGF-E. In particular, Applicants have identified and isolated cDNA encoding a VEGF-E polypeptide, as disclosed in further detail in the Examples below. Using BLAST sequence alignment computer programs, Applicants found that the VEGF-E polypeptide has significant homology with VEGF and bone morphogenetic protein 1. In particular, the cDNA sequence of VEGF-E exhibits 24% amino acid similarity with VEGF and has structural conservation. In addition, VEGF-E contains a N-terminal half which is not present in VEGF and that has 28% homology to bone morphogenetic protein 1.

83. **Full-length PRO285 and PRO286 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO285 and PRO286 In particular, Applicants have identified and isolated cDNAs encoding PRO285 and PRO286 polypeptides, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the coding sequences of PRO285 and PRO286 are highly homologous to DNA sequences HSU88540_1, HSU88878_1, HSU88879_1, HSU88880_1, and HSU88881_1 in the GenBank database.

Accordingly, it is presently believed that the PRO285 and PRO286 proteins disclosed in the present application are newly identified human homologues of the *Drosophila* protein Toll, and are likely to play an important role in adaptive immunity. More specifically, PRO285 and PRO286 may be involved in inflammation, septic shock, and response to pathogens, and play possible roles in diverse medical conditions that are aggravated by immune response, such as, for example, diabetes, ALS, cancer, rheumatoid arthritis, and ulcers. The role of PRO285 and PRO286 as pathogen pattern recognition receptors, sensing the presence of conserved molecular structures present on microbes, is further supported by the data disclosed in the present application, showing that a known human Toll-like receptor, TLR2 is a direct mediator of LPS signaling.

84. **Full-length PRO213-1, PRO1330 and PRO1449 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO213-1, PRO1330 and/or PRO1449. In particular, cDNA encoding a PRO213-1, PRO1330 and/or PRO1449 polypeptide has been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by DNA30943-

1163-1, DNA64907-1163-1 and DNA64908-1163-1 as well as all further native homologues and variants included in the foregoing definition of PRO213-1, PRO1330 and/or PRO1449, will be referred to as "PRO213-1, PRO1330 and/or PRO1449", regardless of their origin or mode of preparation.

85. Full-length PRO298 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO298. (It is noted that PRO298 is an arbitrary designation of a protein encoded by the nucleic acid shown in Figure 218, SEQ ID NO: 514, and having the amino acid sequence shown in Figure 219, SEQ ID NO:515. Further proteins having the same amino acid sequence but expressed in different rounds of expression, may be given different "PRO" numbers.)

In particular, Applicants have identified and isolated cDNA encoding a PRO298 polypeptide, as disclosed in further detail in the Examples below. Using BLASTX 2.0a8MP-WashU computer program, socring parameters: T=12, S=68, S2=36, Matrix: BLOSUM62, Applicants found that the PRO298 protein specifically disclosed herein shows a limited (27-38%) sequence identity with the following sequences found in the GenBank database: S59392 (probable membrane protein YLR246w - yeast); S58154 (hypothetical protein SPAC2F7.10 - yeast); CELF33D11_9 (F33D11.9b - Caenorhabditis elegans); YO41_CAEEL (hypothetical 68.7 kd protein zk757.1); CEAC3_5 (AC3.4 - Caenorhabditis elegans); S52691 (probable transmembrane protein YDR126w - yeast); ATT12H17_14 (protein - Arabidopsis thaliana); S55963 (probable membrane protein YNL326c - yeast); CELC43H6_2 (C43H6.7 - Caenorhabditis elegans); TMO18A10_14 (A_TMO18A10.8 - Arabinosa thaliana).

86. Full-length PRO337 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO337. In particular, Applicants have identified and isolated cDNA encoding a PRO337 polypeptide, as disclosed in further detail in the Examples below. Using BLAST, BLAST-2 and FastA sequence alignment computer programs, Applicants found that a full-length native sequence PRO337 has 97% amino acid sequence identity with rat neurotrimin, 85% sequence identity with chicken CEPU, 73% sequence identity with chicken G55, 59% homology with human LAMP and 84% homology with human OPCAM. Accordingly, it is presently believed that PRO337 disclosed in the present application is a newly identified member of the IgLON sub family of the immunoglobulin superfamily and may possess neurite growth and differentiation potentiating properties.

87. Full-length PRO403 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO403. In particular, Applicants have identified and isolated cDNA encoding a PRO403 polypeptide, as disclosed in further detail in the Examples below. Using a BLAST, BLAST-2 and FastA sequence alignment computer programs, Applicants found that a full-length native sequence PRO403 has 94% identity to bovine ECE-2 and 64% identity to human ECE-1. Accordingly is presently believed that

PRO403 is a new member of the ECE protein family and may posses ability to catalyze the production of active endothelin.

88. PRO Polypeptide Variants

In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO polypeptide variants can be prepared. PRO polypeptide variants can be prepared by introducing appropriate nucleotide changes into the PRO polypeptide DNA, or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO polypeptides, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

Variations in the native full-length sequence PRO polypeptides or in various domains of the PRO polypeptides described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO polypeptide that results in a change in the amino acid sequence of the PRO polypeptide as compared with the native sequence PRO polypeptide. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO polypeptide. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the PRO polypeptide with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity in the *in vitro* assay described in the Examples below.

In particular embodiments, conservative substitutions of interest are shown in Table 1 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 1, or as further described below in reference to amino acid classes, are introduced and the products screened.

Table 1

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	val; leu; ile	val
Arg (R)	lys; gln; asn	lys
Asn (N)	gln; his; lys; arg	gln
Asp (D)	glu	glu
Cys (C)	ser	ser
Gln (Q)	asn	asn
Glu (E)	asp	asp
Gly (G)	pro; ala	ala
His (H)	asn; gln; lys; arg	arg
Ile (I)	leu; val; met; ala; phe; norleucine	leu
Leu (L)	norleucine; ile; val; met; ala; phe	ile
Lys (K)	arg; gln; asn	arg
Met (M)	leu; phe; ile	leu
Phe (F)	leu; val; ile; ala; tyr	leu
Pro (P)	ala	ala
Ser (S)	thr	thr
Thr (T)	ser	ser
Trp (W)	tyr; phe	tyr
Tyr (Y)	trp; phe; thr; ser	phe
Val (V)	ile; leu; met; phe; ala; norleucine	leu

Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

(1) hydrophobic: norleucine, met, ala, val, leu, ile;

(2) neutral hydrophilic: cys, ser, thr;

(3) acidic: asp, glu;

(4) basic: asn, gln, his, lys, arg;

(5) residues that influence chain orientation: gly, pro; and

(6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et

al., Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the desired PRO polypeptide variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

89. Modifications of PRO Polypeptides

Covalent modifications of PRO polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of the PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the PRO polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO polypeptide to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO polypeptide antibodies, and vice-versa. Commonly used crosslinking agents include, *e.g.*, 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)-dithio]propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α-amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the PRO polypeptides included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in a native sequence PRO polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence PRO polypeptide, and/or alteration of the ratio and/or composition of the sugar residues attached to the glycosylation site(s).

Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO polypeptide (for O-linked glycosylation sites). The PRO

polypeptide amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO polypeptide polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of PRO polypeptides of the invention comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, *e.g.*, polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The PRO polypeptides of the present invention may also be modified in a way to form a chimeric molecule comprising a PRO polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of the PRO polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the PRO polypeptide. The presence of such epitope-tagged forms of the PRO polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an α-tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

90. Preparation of PRO Polypeptides

The description below relates primarily to production of PRO polypeptides by culturing cells transformed or transfected with a vector containing the desired PRO polypeptide nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare the PRO polypeptide. For instance, the PRO polypeptide sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the desired PRO polypeptide may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO polypeptide.

A. Isolation of DNA Encoding PRO Polypeptides

DNA encoding PRO polypeptides may be obtained from a cDNA library prepared from tissue believed to possess the desired PRO polypeptide mRNA and to express it at a detectable level. Accordingly, human PRO polypeptide DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO polypeptide-encoding gene may also be obtained from a genomic library or by oligonucleotide synthesis.

Libraries can be screened with probes (such as antibodies to the desired PRO polypeptide or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding the desired PRO polypeptide is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer:A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ^{32}P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined through sequence alignment using computer software programs such as BLAST, ALIGN, DNAstar, and INHERIT which employ various algorithms to measure homology.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic

libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

B. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for PRO polypeptide production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of transfection are known to the ordinarily skilled artisan, for example, $CaPO_4$ and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes or other cells that contain substantial cell-wall barriers. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transformations have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, *e.g.*, polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, *e.g.*, *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, *e.g.*, *Salmonella typhimurium*, *Serratia*, *e.g.*, *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (*e.g.*, *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325); and K5 772 (ATCC 53,635). These examples are illustrative rather than limiting. Strain W3110 is

one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA* ; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC 55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan'*; *E. coli* W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan'*; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, *e.g.*, PCR or other nucleic acid polymerase reactions, are suitable.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO polypeptide-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer *et al.*, Bio/Technology, 9: 968-975 (1991)) such as, *e.g.*, *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt *et al.*, J. Bacteriol., 737 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickeramii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilarum* (ATCC 36,906; Van den Berg *et al.*, Bio/Technology, 8: 135 (1990)), *K. thermotolerans*, and *K. marxianus; yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna *et al.*, J. Basic Microbiol., 28: 265-278 [1988]); *Candida; Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case *et al.*, Proc. Natl. Acad. Sci. USA, 76: 5259-5263 [1979]); *Schwanniomyces* such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, *e.g.*, *Neurospora, Penicillium, Tolypocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance *et al.*, Biochem. Biophys. Res. Commun., 112: 284-289 [1983]; Tilburn *et al.*, Gene, 26: 205-221 [1983]; Yelton *et al.*, Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4: 475-479 [1985]). Methylotropic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula, Candida, Kloeckera, Pichia, Saccharomyces, Torulopsis,* and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylotrophs, 269 (1982).

Suitable host cells for the expression of glycosylated PRO polypeptides are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as Drosophila S2 and Spodoptera Sf9, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol., 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

C. Selection and Use of a Replicable Vector

The nucleic acid (*e.g.*, cDNA or genomic DNA) encoding a desired PRO polypeptide may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

The PRO polypeptide of interest may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO polypeptide DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α-factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, *e.g.*, ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, *e.g.*, the gene encoding D-alanine racemase for *Bacilli*.

An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO polypeptide nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp*1 gene present in the yeast plasmid YRp7 [Stinchcomb et al., Nature, 282:39 (1979); Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)]. The *trp*1 gene

provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, Genetics, 85:12 (1977)].

Expression and cloning vectors usually contain a promoter operably linked to the PRO polypeptide nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β-lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (trp) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid promoters such as the tac promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding the desired PRO polypeptide.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., J. Biol. Chem., 255:2073 (1980)] or other glycolytic enzymes [Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

PRO polypeptide transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, *e.g.*, the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding the desired PRO polypeptide by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α-fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO polypeptide coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of

transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO polypeptides.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO polypeptides in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.

D. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to a PRO polypeptide DNA and encoding a specific antibody epitope.

E. Purification of Polypeptide

Forms of PRO polypeptides may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (*e.g.* Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO polypeptides can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify PRO polypeptides from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO polypeptide. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182

(1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO polypeptide produced.

91. Uses for PRO Polypeptides

Nucleotide sequences (or their complement) encoding the PRO polypeptides of the present invention have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO polypeptide-encoding nucleic acid will also be useful for the preparation of PRO polypeptides by the recombinant techniques described herein.

The full-length native sequence PRO polypeptide-encoding nucleic acid or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length PRO polypeptide gene or to isolate still other genes (for instance, those encoding naturally-occurring variants of the PRO polypeptide or PRO polypeptides from other species) which have a desired sequence identity to the PRO polypeptide nucleic acid sequences. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from the nucleotide sequence of any of the DNA molecules disclosed herein or from genomic sequences including promoters, enhancer elements and introns of native sequence PRO polypeptide encoding DNA. By way of example, a screening method will comprise isolating the coding region of the PRO polypeptide gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, including radionucleotides such as ^{32}P or ^{35}S, or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the specific PRO polypeptide gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

The ESTs disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO polypeptide sequences.

Nucleotide sequences encoding a PRO polypeptide can also be used to construct hybridization probes for mapping the gene which encodes that PRO polypeptide and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

When the coding sequence for the PRO polypeptide encodes a protein which binds to another protein, the PRO polypeptide can be used in assays to identify its ligands. Similarly, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Screening assays can be designed to find lead compounds that mimic the biological activity of a native PRO polypeptide or a ligand for the PRO

polypeptide. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

Nucleic acids which encode a PRO polypeptide or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding a PRO polypeptide of interest can be used to clone genomic DNA encoding the PRO polypeptide in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding the PRO polypeptide. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for PRO polypeptide transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding a PRO polypeptide introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding the PRO polypeptide. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of PRO polypeptides can be used to construct a PRO polypeptide "knock out" animal which has a defective or altered gene encoding the PRO polypeptide of interest as a result of homologous recombination between the endogenous gene encoding the PRO polypeptide and altered genomic DNA encoding the PRO polypeptide introduced into an embryonic cell of the animal. For example, cDNA encoding a PRO polypeptide can be used to clone genomic DNA encoding the PRO polypeptide in accordance with established techniques. A portion of the genomic DNA encoding a PRO polypeptide can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, Cell, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., Cell, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can

then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the PRO polypeptide.

When *in vivo* administration of a PRO polypeptide is employed, normal dosage amounts may vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1 μg/kg/day to 10 mg/kg/day, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature; see, for example, U.S. Pat. Nos. 4,657,760; 5,206,344; or 5,225,212. It is anticipated that different formulations will be effective for different treatment compounds and different disorders, that administration targeting one organ or tissue, for example, may necessitate delivery in a manner different from that to another organ or tissue.

Where sustained-release administration of a PRO polypeptide is desired in a formulation with release characteristics suitable for the treatment of any disease or disorder requiring administration of the PRO polypeptide, microencapsulation of the PRO polypeptide is contemplated. Microencapsulation of recombinant proteins for sustained release has been successfully performed with human growth hormone (rhGH), interferon- (rhIFN-), interleukin-2, and MN rgp120. Johnson *et al.*, Nat. Med., 2: 795-799 (1996); Yasuda, Biomed. Ther., 27: 1221-1223 (1993); Hora *et al.*, Bio/Technology, 8: 755-758 (1990); Cleland, "Design and Production of Single Immunization Vaccines Using Polylactide Polyglycolide Microsphere Systems," in Vaccine Design: The Subunit and Adjuvant Approach, Powell and Newman, eds, (Plenum Press: New York, 1995), pp. 439-462; WO 97/03692, WO 96/40072, WO 96/07399; and U.S Pat. No. 5,654,010.

The sustained-release formulations of these proteins were developed using poly-lactic-coglycolic acid (PLGA) polymer due to its biocompatibility and wide range of biodegradable properties. The degradation products of PLGA, lactic and glycolic acids, can be cleared quickly within the human body. Moreover, the degradability of this polymer can be adjusted from months to years depending on its molecular weight and composition. Lewis, "Controlled release of bioactive agents from lactide/glycolide polymer," in: M. Chasin and R. Langer (Eds.), Biodegradable Polymers as Drug Delivery Systems (Marcel Dekker: New York, 1990), pp. 1-41.

For example, for a formulation that can provide a dosing of approximately 80 g/kg/day in mammals with a maximum body weight of 85 kg, the largest dosing would be approximately 6.8 mg of the PRO polypeptide per day. In order to achieve this dosing level, a sustained- release formulation which contains a maximum possible protein loading (15-20% w/w PRO polypeptide) with the lowest possible initial burst (<20%) is necessary. A continuous (zero-order) release of the PRO polypeptide from microparticles for 1-2 weeks is also desirable. In addition, the encapsulated protein to be released should maintain its integrity and stability over the desired release period.

PRO213 polypeptides and portions thereof which possess the ability to regulate the growth induction

cascade and/or the blood coagulation cascade may also be employed for such purposes both *in vivo* therapy and *in vitro*. Those of ordinary skill in the art will well know how to employ PRO213 polypeptides for such uses.

PRO274 polypeptides and portions thereof which have homology to 7TM protein and Fn54 may also be useful for *in vivo* therapeutic purposes, as well as for various other applications. The identification of novel 7TM protein and Fn54-like molecules may have relevance to a number of human disorders which involve recognition of ligands and the subsequent signal transduction of information contained within those ligands in order to control cellular processes. Thus, the identification of new 7TM protein and Fn54-like molecules is of special importance in that such proteins may serve as potential therapeutics for a variety of different human disorders. Such polypeptides may also play important roles in biotechnological and medical research as well as in various industrial applications. As a result, there is particular scientific and medical interest in new molecules, such as PRO274.

PRO300 polypeptides and portions thereof which have homology to Diff 33 may also be useful for *in vivo* therapeutic purposes, as well as for various other applications. The identification of novel Diff 33-like molecules may have relevance to a number of human disorders such as the physiology of cancer. Thus, the identification of new Diff 33-like molecules is of special importance in that such proteins may serve as potential therapeutics for a variety of different human disorders. Such polypeptides may also play important roles in biotechnological and medical research as well as various industrial applications. As a result, there is particular scientific and medical interest in new molecules, such as PRO300.

PRO296 polypeptides of the present invention which possess biological activity related to that of the sarcoma-amplified SAS protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO296 polypeptides of the present invention for such purposes.

PRO329 polypeptides of the present invention which possess biological activity related to that of immunoglobulin F_c receptor protein or subunit thereof may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO329 polypeptides of the present invention for such purposes.

PRO362 polypeptides of the present invention which possess biological activity related to that of the A33 antigen protein, HCAR protein or the NrCAM related cell adhesion molecule may be employed both *in vivo* for therapeutic purposes and *in vitro*.

PRO363 polypeptides of the present invention which possess biological activity related to that of the cell surface HCAR protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO363 polypeptides of the present invention for such purposes. Specifically, extracellular domains derived from the PRO363 polypeptides may be employed therapeutically *in vivo* for lessening the effects of viral infection.

PRO868 polypeptides of the present invention which possess biological activity related to that of the tumor necrosis factor protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO868 polypeptides of the present invention for such

purposes.

PRO382 polypeptides of the present invention which possess biological activity related to that of the serine protease proteins may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO382 polypeptides of the present invention for such purposes.

PRO545 polypeptides and portions thereof which have homology to meltrin may also be useful for *in vivo* therapeutic purposes, as well as for various other applications. The identification of novel molecules associated with cellular adhesion may be relevant to a number of human disorders. Given that the meltrin proteins may play an important role in a number of disease processes, the identification of new meltrin proteins and meltrin-like molecules is of special importance in that such proteins may serve as potential therapeutics for a variety of different human disorders. Such polypeptides may also play important roles in biotechnological and medical research, as well as various industrial applications. As a result, there is particular scientific and medical interest in new molecules, such as PRO545.

PRO617 polypeptides of the present invention which possess biological activity related to that of the CD24 protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO617 polypeptides of the present invention for such purposes.

PRO700 polypeptides and portions thereof which have homology to protein disulfide isomerase may also be useful for *in vivo* therapeutic purposes, as well as for various other applications. The identification of novel protein disulfide isomerases and related molecules may be relevant to a number of human disorders. Given that formation of disulfide bonds and protein folding play important roles in a number of biological processes, the identification of new protein disulfide isomerases and protein disulfide isomerase-like molecules is of special importance in that such proteins may serve as potential therapeutics for a variety of different human disorders. Such polypeptides may also play important roles in biotechnological and medical research, as well as various industrial applications. As a result, there is particular scientific and medical interest in new molecules, such as PRO700.

PRO702 polypeptides of the present invention which possess biological activity related to that of the conglutinin protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO702 polypeptides of the present invention for such purposes. PRO702 polypeptides having conglutinin activity would be expected to be capable of inhibiting haemagglutinin activity by influenza viruses and/or function as immunoglobulin-independent defense molecules as a result of a complement-mediated mechanism.

PRO703 polypeptides of the present invention which possess biological activity related to that of the VLCAS protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO703 polypeptides of the present invention for such purposes.

PRO703 polypeptides and portions thereof which have homology to VLCAS may also be useful for *in vivo* therapeutic purposes, as well as for various other applications. The identification of novel VLCAS proteins and related molecules may be relevant to a number of human disorders. Thus, the identification of new VLCAS

proteins and VLCAS protein-like molecules is of special importance in that such proteins may serve as potential therapeutics for a variety of different human disorders. Such polypeptides may also play important roles in biotechnological and medical research as well as various industrial applications. As a result, there is particular scientific and medical interest in new molecules, such as PRO703.

PRO705 polypeptides of the present invention which possess biological activity related to that of the K-glypican protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO705 polypeptides of the present invention for such purposes.

PRO708 polypeptides of the present invention which possess biological activity related to that of the aryl sulfatase proteins may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO708 polypeptides of the present invention for such purposes.

PRO320 polypeptides of the present invention which possess biological activity related to that of the fibulin protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO320 polypeptides of the present invention for such purposes.

PRO320 polypeptides and portions thereof which have homology to fibulin may also be useful for *in vivo* therapeutic purposes, as well as for various other applications. The identification of novel fibulin proteins and related molecules may be relevant to a number of human disorders such as cancer or those involving connective tissue, attachment molecules and related mechanisms. Thus, the identification of new fibulin proteins and fibulin protein-like molecules is of special importance in that such proteins may serve as potential therapeutics for a variety of different human disorders. Such polypeptides may also play important roles in biotechnological and medical research as well as various industrial applications. As a result, there is particular scientific and medical interest in new molecules, such as PRO320.

PRO324 polypeptides of the present invention which possess biological activity related to that of oxidoreductases may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO324 polypeptides of the present invention for such purposes.

PRO351 polypeptides of the present invention which possess biological activity related to that of the prostasin protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO351 polypeptides of the present invention for such purposes.

PRO351 polypeptides and portions thereof which have homology to prostasin may also be useful for *in vivo* therapeutic purposes, as well as for various other applications. The identification of novelprostasin proteins and related molecules may be relevant to a number of human disorders. Thus, the identification of new prostasin proteins and prostasin -like molecules is of special importance in that such proteins may serve as potential therapeutics for a variety of different human disorders. Such polypeptides may also play important roles in biotechnological and medical research as well as various industrial applications. As a result, there is particular scientific and medical interest in new molecules, such as PRO351.

PRO352 polypeptides of the present invention which possess biological activity related to that of the butyrophilin protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO352 polypeptides of the present invention for such purposes.

PRO381 polypeptides of the present invention which possess biological activity related to that of one or more of the FKPB immunophilin proteins may be employed both *in vivo* for therapeutic purposes and *in vitro*, for example for enhancing immunosuppressant activity and/or for axonal regeneration. Those of ordinary skill in the art will well know how to employ the PRO381 polypeptides of the present invention for such purposes.

PRO386 polypeptides of the present invention which possess biological activity related to that of the beta-2 subunit of a sodium channel expressed in mammalian cells may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO386 polypeptides of the present invention for such purposes.

PRO540 polypeptides of the present invention which possess biological activity related to that of the LCAT protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO540 polypeptides of the present invention for such purposes.

PRO615 polypeptides of the present invention which possess biological activity related to that of the synaptogyrin protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO615 polypeptides of the present invention for such purposes.

PRO615 polypeptides and portions thereof which have homology to synaptogyrin may also be useful for *in vivo* therapeutic purposes, as well as for various other applications. The identification of novel synaptogyrin proteins and related molecules may be relevant to a number of human disorders. Thus, the identification of new synaptogyrin proteins and synaptogyrin-like molecules is of special importance in that such proteins may serve as potential therapeutics for a variety of different human disorders. Such polypeptides may also play important roles in biotechnological and medical research as well as various industrial applications. As a result, there is particular scientific and medical interest in new molecules, such as PRO615.

PRO618 polypeptides of the present invention which possess biological activity related to that of an enteropeptidase may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO618 polypeptides of the present invention for such purposes.

PRO618 polypeptides and portions thereof which have homology to enteropeptidase may also be useful for *in vivo* therapeutic purposes, as well as for various other applications. The identification of novel enteropeptidase proteins and related molecules may be relevant to a number of human disorders. Thus, the identification of new enteropeptidase proteins and enteropeptidase-like molecules is of special importance in that such proteins may serve as potential therapeutics for a variety of different human disorders. Such polypeptides may also play important roles in biotechnological and medical research as well as various industrial applications. As a result, there is particular scientific and medical interest in new molecules, such as PRO618.

PRO719 polypeptides of the present invention which possess biological activity related to that of the lipoprotein lipase H protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO719 polypeptides of the present invention for such purposes.

PRO724 polypeptides of the present invention which possess biological activity related to that of the human LDL receptor protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of

ordinary skill in the art will well know how to employ the PRO724 polypeptides of the present invention for such purposes.

PRO772 polypeptides of the present invention which possess biological activity related to that of the human A4 protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO772 polypeptides of the present invention for such purposes.

PRO852 polypeptides of the present invention which possess biological activity related to that of certain protease protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO852 polypeptides of the present invention for such purposes.

PRO853 polypeptides of the present invention which possess biological activity related to that of the reductase protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO853 polypeptides of the present invention for such purposes.

PRO853 polypeptides and portions thereof which have homology to reductase proteins may also be useful for *in vivo* therapeutic purposes, as well as for various other applications. Given that oxygen free radicals and antioxidants appear to play important roles in a number of disease processes, the identification of new reductase proteins and reductase-like molecules is of special importance in that such proteins may serve as potential therapeutics for a variety of different human disorders. Such polypeptides may also play important roles in biotechnological and medical research as well as various industrial applications. As a result, there is particular scientific and medical interest in new molecules, such as PRO853.

PRO860 polypeptides of the present invention which possess biological activity related to that of the neurofascin protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO860 polypeptides of the present invention for such purposes.

PRO860 polypeptides and portions thereof which have homology to neurofascin may also be useful for *in vivo* therapeutic purposes, as well as for various other applications. The identification of novel neurofascin proteins and related molecules may be relevant to a number of human disorders which involve cellular adhesion. Thus, the identification of new neurofascin proteins and neurofascin protein-like molecules is of special importance in that such proteins may serve as potential therapeutics for a variety of different human disorders. Such polypeptides may also play important roles in biotechnological and medical research as well as various industrial applications. As a result, there is particular scientific and medical interest in new molecules, such as PRO860.

PRO846 polypeptides of the present invention which possess biological activity related to that of the CMRF35 protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO846 polypeptides of the present invention for such purposes.

PRO846 polypeptides and portions thereof which have homology to the CMRF35 protein may also be useful for *in vivo* therapeutic purposes, as well as for various other applications. The identification of novel CMRF35 protein and related molecules may be relevant to a number of human disorders. Thus, the identification of new CMRF35 protein and CMRF35 protein-like molecules is of special importance in that such proteins may serve as potential therapeutics for a variety of different human disorders. Such polypeptides may

also play important roles in biotechnological and medical research as well as various industrial applications. As a result, there is particular scientific and medical interest in new molecules, such as PRO846.

PRO862 polypeptides of the present invention which possess biological activity related to that of the lysozyme protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO862 polypeptides of the present invention for such purposes.

PRO862 polypeptides and portions thereof which have homology to the lysozyme protein may also be useful for *in vivo* therapeutic purposes, as well as for various other applications. The identification of novel lysozyme proteins and related molecules may be relevant to a number of human disorders. Thus, the identification of new lysozymes and lysozyme-like molecules is of special importance in that such proteins may serve as potential therapeutics for a variety of different human disorders. Such polypeptides may also play important roles in biotechnological and medical research as well as various industrial applications. As a result, there is particular scientific and medical interest in new molecules, such as PRO862.

PRO864 polypeptides of the present invention which possess biological activity related to that of the Wnt-4 protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO864 polypeptides of the present invention for such purposes.

PRO864 polypeptides and portions thereof which have homology to the Wnt-4 protein may also be useful for *in vivo* therapeutic purposes, as well as for various other applications. The identification of novel Wnt-4 proteins and related molecules may be relevant to a number of human disorders. Thus, the identification of new Wnt-4 protein and Wnt-4 protein-like molecules is of special importance in that such proteins may serve as potential therapeutics for a variety of different human disorders. Such polypeptides may also play important roles in biotechnological and medical research as well as various industrial applications. As a result, there is particular scientific and medical interest in new molecules, such as PRO864.

PRO792 polypeptides of the present invention which possess biological activity related to that of the CD23 protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO792 polypeptides of the present invention for such purposes.

PRO866 polypeptides of the present invention which possess biological activity related to that of mindin and/or spondin protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO866 polypeptides of the present invention for such purposes.

PRO871 polypeptides of the present invention which possess biological activity related to that of the cyclophilin protein family may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO871 polypeptides of the present invention for such purposes.

PRO873 polypeptides of the present invention which possess biological activity related to that of carboxylesterases may be employed both *in vivo* for therapeutic purposes and *in vitro*. For example, they be used in conjunction with prodrugs to convert the prodrug to its active form (see Danks *et al., supra*). They may be used to inhibit parasite infection (see van Pelt *et al., supra*). Methods for employ the PRO873 polypeptides

of the present invention for these, and other purposes will be readily apparent to those of ordinary skill in the art.

PRO940 polypeptides of the present invention which possess biological activity related to that of the CD33 protein and/or OB binding protein-2 may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO940 polypeptides of the present invention for such purposes.

PRO941 polypeptides of the present invention which possess biological activity related to that of a cadherin protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO941 polypeptides of the present invention for such purposes.

PRO944 polypeptides of the present invention which possess biological activity related to that of the CPE-R protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO944 polypeptides of the present invention for such purposes. PRO944 polypeptides of the present invention that function to bind to Clostridium perfringens enterotoxin (CPE) may find use for effectively treating infection by the CPE endotoxin.

PRO983 polypeptides of the present invention which possess biological activity related to that of the vesicle-associated membrane protein, VAP-33, may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO983 polypeptides of the present invention for such purposes.

PRO1057 polypeptides of the present invention which possess biological activity related to that of protease proteins may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO1057 polypeptides of the present invention for such purposes.

PRO1071 polypeptides of the present invention which possess biological activity related to that of the thrombospondin protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO1071 polypeptides of the present invention for such purposes.

PRO1072 polypeptides of the present invention which possess biological activity related to that of reductase proteins may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO1072 polypeptides of the present invention for such purposes.

PRO1075 polypeptides of the present invention which possess biological activity related to that of protein disulfide isomerase may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO1075 polypeptides of the present invention for such purposes.

PRO181 polypeptides of the present invention which possess biological activity related to that of the cornichon protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO181 polypeptides of the present invention for such purposes.

PRO827 polypeptides of the present invention which possess biological activity related to that of various integrin proteins may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill

in the art will well know how to employ the PRO827 polypeptides of the present invention for such purposes.

PRO1114 polypeptides of the present invention which possess biological activity related to that of the cytokine receptor family of proteins may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO1114 polypeptides of the present invention for such purposes.

In addition to the above, the PRO1114 interferon receptor polypeptides may be employed in applications, both *in vivo* and *in vitro*, where the ability to bind to an interferon ligand is desired. Such applications will be well within the skill level in the art.

PRO237 polypeptides of the present invention which possess biological activity related to that of the carbonic anhydrase protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO237 polypeptides of the present invention for such purposes.

PRO541 polypeptides of the present invention which possess biological activity related to that of a trypsin inhibitor protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO541 polypeptides of the present invention for such purposes.

PRO273 polypeptides can be used in assays that other chemokines would be used in to perform comparative assays. The results can be used accordingly.

PRO701 polypeptides of the present invention which possess biological activity related to that of the neuroligin family may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO701 polypeptides of the present invention for such purposes.

PRO701 can be used in assays with neurons and its activity thereon can be compared with that of neuroligins 1, 2 and 3. The results can be applied accordingly.

PRO704 polypeptides of the present invention which possess biological activity related to that of vesicular integral membrane proteins may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO704 polypeptides of the present invention for such purposes.

PRO704 can be used in assays with the polypeptides to which they have identity with to determine the relative activities. The results can be applied accordingly. PRO704 can be tagged or measured for activity to measure endocytosis activity and thereby used to screen for agents which effect endocytosis.

PRO706 polypeptides of the present invention which possess biological activity related to that of the endogenous prostatic acid phosphatase precursor may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO706 polypeptides of the present invention for such purposes.

PRO706 can be used in assays with human prostatic acid phosphatase or human lysosomal acid phosphatase and its activity thereon can be compared with that of human prostatic acid phosphatase or human lysosomal acid phosphatase. The results can be applied accordingly.

PRO707 polypeptides of the present invention which possess biological activity related to that of cadherins may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO707 polypeptides of the present invention for such purposes.

PRO707 can be used in assays to determine its activity in relation to other cadherins, particularly cadherin FIB3. The results can be applied accordingly.

PRO322 polypeptides of the present invention which possess biological activity related to that of neuropsin may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO322 polypeptides of the present invention for such purposes.

PRO322 can be used in assays to determine its activity relative to neuropsin, trypsinogen, serine protease and neurosin, and the results applied accordingly.

PRO526 polypeptides of the present invention which possess biological activity related to that of protein-protein binding proteins may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO526 polypeptides of the present invention for such purposes.

Assays can be performed with growth factors and other proteins which are known to form complexes to determine whether PRO526 binds thereto and whether there is increased half-life due to such binding. The results can be used accordingly.

PRO531 polypeptides of the present invention which possess biological activity related to that of the protocadherins may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO531 polypeptides of the present invention for such purposes.

PRO531 can be used in assays against protocadherin 3 and other protocadherins, to determine their relative activities. The results can be applied accordingly.

PRO534 polypeptides of the present invention which possess biological activity related to that of the protein disulfide isomerase may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO534 polypeptides of the present invention for such purposes.

PRO534 can be used in assays with protein disulfide isomerase to determine the relative activities. The results can be applied accordingly.

PRO697 polypeptides of the present invention which possess biological activity related to that of the sFRP family may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO697 polypeptides of the present invention for such purposes.

PRO697 can be used in assays with sFRPs and SARPs to determine the relative activities. The results can be applied accordingly.

PRO731 polypeptides of the present invention which possess biological activity related to that of any protocadherin may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO731 polypeptides of the present invention for such purposes.

PRO731 can be used in assays with the polypeptides to which they have identity with to determine the

relative activities. The results can be applied accordingly.

PRO768 polypeptides of the present invention which possess biological activity related to that of integrins may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO768 polypeptides of the present invention for such purposes.

PRO768 can be used in assays with the polypeptides to which they have identity with to determine the relative activities. The results can be applied accordingly.

PRO771 polypeptides of the present invention which possess biological activity related to that of the testican protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO771 polypeptides of the present invention for such purposes.

PRO771 can be used in assays with the polypeptides to which they have identity with to determine the relative activities. The results can be applied accordingly.

PRO733 polypeptides of the present invention which possess biological activity related to that of the proteins which bind the T1/ST2 receptor may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO733 polypeptides of the present invention for such purposes.

PRO733 can be used in assays with the polypeptides to which they have identity with to determine the relative activities. The results can be applied accordingly.

PRO162 polypeptides of the present invention which possess biological activity related to that of the pancreatitis-associated protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO162 polypeptides of the present invention for such purposes.

PRO162 can be used in assays with the polypeptides to which they have identity with to determine the relative activities. The results can be applied accordingly.

PRO788 polypeptides of the present invention which possess biological activity related to that of the anti-neoplastic urinary protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO788 polypeptides of the present invention for such purposes.

PRO788 can be used in assays with the polypeptides to which they have identity with to determine the relative activities. The results can be applied accordingly.

PRO1008 polypeptides of the present invention which possess biological activity related to that of dkk-1 may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO1008 polypeptides of the present invention for such purposes.

PRO1008 can be used in assays with the polypeptides to which they have identity with to determine the relative activities. The results can be applied accordingly.

PRO1012 polypeptides of the present invention which possess biological activity related to that of the protein disulfide isomerase may be employed both *in vivo* and *in vitro* purposes. Those of ordinary skill in the art will well know how to employ the PRO1012 polypeptides of the present invention for such purposes.

PRO1012 can be used in assays with the polypeptides to which they have identity with to determine the relative activities. The results can be applied accordingly.

PRO1014 polypeptides of the present invention which possess biological activity related to that of reductase may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO1014 polypeptides of the present invention for such purposes.

PRO1014 can be used in assays with the polypeptides to which they have identity with to determine the relative activities. Inhibitors of PRO1014 are particularly preferred. The results can be applied accordingly.

PRO1017 polypeptides of the present invention which possess biological activity related to that of sulfotransferase may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO1017 polypeptides of the present invention for such purposes.

PRO1017 can be used in assays with the polypeptides to which they have identity with to determine the relative activities. The results can be applied accordingly.

PRO474 polypeptides of the present invention which possess biological activity related to that of dehydrogenase may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO474 polypeptides of the present invention for such purposes.

PRO474 can be used in assays with the polypeptides to which they have identity with to determine the relative activities. The results can be applied accordingly.

PRO1031 polypeptides of the present invention which possess biological activity related to that of IL-17 may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO1031 polypeptides of the present invention for such purposes.

PRO1031 can be used in assays with the polypeptides to which they have identity with to determine the relative activities. The results can be applied accordingly.

PRO938 polypeptides of the present invention which possess biological activity related to that of protein disulfide isomerase may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO938 polypeptides of the present invention for such purposes.

PRO1082 polypeptides of the present invention which possess biological activity related to that of the LDL receptor may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO1082 polypeptides of the present invention for such purposes.

PRO1082 can be used in assays with the polypeptides to which they have identity with to determine the relative activities. The results can be applied accordingly. PRO1082 can also be used in assays to identify candidate agents which modulate the receptors.

PRO1083 polypeptides of the present invention which possess biological activity related to that of 7TM receptors may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO1083 polypeptides of the present invention for such purposes.

In particular PRO1083 can be used in assays to determine candidate agents which control or modulate PRO1083, i.e., have an effect on the receptor.

The VEGF-E molecules herein have a number of therapeutic uses associated with survival, proliferation

and/or differention of cells. Such uses include the treatment of umbilical vein endothelial cells, in view of the demonstrated ability of VEGF-E to increase survival of human umbilical vein endothelial cells. Treatment may be needed if the vein were subjected to traumata, or situations wherein artificial means are employed to enhance the survival of the umbilical vein, for example, where it is weak, diseased, based on an artificial matrix, or in an artificial environment. Other physiological conditions that could be improved based on the selective mitogenic character of VEGF-E are also included herein. Uses also include the treatment of fibroblasts and myocytes, in view of the demonstrated ability of VEGF-E to induce proliferation of fibroblasts and hypertrophy in myocytes. In particular, VEGF-E can be used in wound healing, tissue growth and muscle generation and regeneration.

For the indications referred to above, the VEGF-E molecule will be formulated and dosed in a fashion consistent with good medical practice taking into account the specific disorder to be treated, the condition of the individual patient, the site of delivery of the VEGF-E, the method of administration, and other factors known to practitioners. Thus, for purposes herein, the "therapeutically effective amount" of the VEGF-E is an amount that is effective either to prevent, lessen the worsening of, alleviate, or cure the treated condition, in particular that amount which is sufficient to enhance the survival, proliferation and/or differentiation of the treated cells in vivo.

VEGF-E amino acid variant sequences and derivatives that are immunologically crossreactive with antibodies raised against native VEGF are useful in immunoassays for VEGF-E as standards, or, when labeled, as competitive reagents.

The VEGF-E is prepared for storage or administration by mixing VEGF-E having the desired degree of purity with physiologically acceptable carriers, excipients, or stabilizers. Such materials are non-toxic to recipients at the dosages and concentrations employed. If the VEGF-E is water soluble, it may be formulated in a buffer such as phosphate or other organic acid salt preferably at a pH of about 7 to 8. If the VEGF-E is only partially soluble in water, it may be prepared as a microemulsion by formulating it with a nonionic surfactant such as Tween, Pluronics, or PEG, e.g., Tween 80, in an amount of 0.04-0.05% (w/v), to increase its solubility.

Optionally other ingredients may be added such as antioxidants, e.g., ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, mannose, or dextrins; chelating agents such as EDTA; and sugar alcohols such as mannitol or sorbitol.

The VEGF-E to be used for therapeutic administration must be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). The VEGF-E ordinarily will be stored in lyophilized form or as an aqueous solution if it is highly stable to thermal and oxidative denaturation. The pH of the VEGF-E preparations typically will be about from 6 to 8, although higher or lower pH values may also be appropriate in certain instances. It will be understood that use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of salts of the VEGF-E.

If the VEGF-E is to be used parenterally, therapeutic compositions containing the VEGF-E generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Generally, where the disorder permits, one should formulate and dose the VEGF-E for site-specific delivery. This is convenient in the case of wounds and ulcers.

Sustained release formulations may also be prepared, and include the formation of microcapsular particles and implantable articles. For preparing sustained-release VEGF-E compositions, the VEGF-E is preferably incorporated into a biodegradable matrix or microcapsule. A suitable material for this purpose is a polylactide, although other polymers of poly-(a-hydroxycarboxylic acids), such as poly-D-(-)-3-hydroxybutyric acid (EP 133,988A), can be used. Other biodegradable polymers include poly(lactones), poly(acetals), poly(orthoesters), or poly(orthocarbonates). The initial consideration here must be that the carrier itself, or its degradation products, is nontoxic in the target tissue and will not further aggravate the condition. This can be determined by routine screening in animal models of the target disorder or, if such models are unavailable, in normal animals. Numerous scientific publications document such animal models.

For examples of sustained release compositions, see U.S. Patent No. 3,773,919, EP 58,481A, U.S. Patent No. 3,887,699, EP 158,277A, Canadian Patent No. 1176565, U. Sidman *et al.*, *Biopolymers 22*, 547 [1983], and R. Langer *et al.*, *Chem. Tech. 12*, 98 [1982].

When applied topically, the VEGF-E is suitably combined with other ingredients, such as carriers and/or adjuvants. There are no limitations on the nature of such other ingredients, except that they must be pharmaceutically acceptable and efficacious for their intended administration, and cannot degrade the activity of the active ingredients of the composition. Examples of suitable vehicles include ointments, creams, gels, or suspensions, with or without purified collagen. The compositions also may be impregnated into transdermal patches, plasters, and bandages, preferably in liquid or semi-liquid form.

For obtaining a gel formulation, the VEGF-E formulated in a liquid composition may be mixed with an effective amount of a water-soluble polysaccharide or synthetic polymer such as polyethylene glycol to form a gel of the proper viscosity to be applied topically. The polysaccharide that may be used includes, for example, cellulose derivatives such as etherified cellulose derivatives, including alkyl celluloses, hydroxyalkyl celluloses, and alkylhydroxyalkylcelluloses, for example, methylcellulose, hydroxyethyl cellulose, carboxymethyl cellulose, hydroxypropyl methylcellulose, and hydroxypropyl cellulose; starch and fractionated starch; agar; alginic acid and alginates; gum arabic; pullullan; agarose; carrageenan; dextrans; dextrins; fructans; inulin; mannans; xylans; arabinans; chitosans; glycogens; glucans; and synthetic biopolymers; as well as gums such as xanthan gum; guar gum; locust bean gum; gum arabic; tragacanth gum; and karaya gum; and derivatives and mixtures thereof. The preferred gelling agent herein is one that is inert to biological systems, nontoxic, simple to prepare, and not too runny or viscous, and will not destabilize the VEGF-E held within it.

Preferably the polysaccharide is an etherified cellulose derivative, more preferably one that is well defined, purified, and listed in USP, e.g., methylcellulose and the hydroxyalkyl cellulose derivatives, such as hydroxypropyl cellulose, hydroxyethyl cellulose, and hydroxypropyl methylcellulose. Most preferred herein

is methylcellulose.

The polyethylene glycol useful for gelling is typically a mixture of low and high molecular weight polyethylene glycols to obtain the proper viscosity. For example, a mixture of a polyethylene glycol of molecular weight 400-600 with one of molecular weight 1500 would be effective for this purpose when mixed in the proper ratio to obtain a paste.

The term "water soluble" as applied to the polysaccharides and polyethylene glycols is meant to include colloidal solutions and dispersions. In general, the solubility of the cellulose derivatives is determined by the degree of substitution of ether groups, and the stabilizing derivatives useful herein should have a sufficient quantity of such ether groups per anhydroglucose unit in the cellulose chain to render the derivatives water soluble. A degree of ether substitution of at least 0.35 ether groups per anhydroglucose unit is generally sufficient. Additionally, the cellulose derivatives may be in the form of alkali metal salts, for example, the Li, Na, K, or Cs salts.

If methylcellulose is employed in the gel, preferably it comprises about 2-5%, more preferably about 3%, of the gel and the VEGF is present in an amount of about 300-1000 mg per ml of gel.

The dosage to be employed is dependent upon the factors described above. As a general proposition, the VEGF-E is formulated and delivered to the target site or tissue at a dosage capable of establishing in the tissue a VEGF-E level greater than about 0.1 ng/cc up to a maximum dose that is efficacious but not unduly toxic. This intra-tissue concentration should be maintained if possible by continuous infusion, sustained release, topical application, or injection at empirically determined frequencies.

It is within the scope hereof to combine the VEGF-E therapy with other novel or conventional therapies (e.g., growth factors such as VEGF, aFGF, bFGF, PDGF, IGF, NGF, anabolic steroids, EGF or TGF-a) for enhancing the activity of any of the growth factors, including VEGF-E, in promoting cell proliferation, survival, differentiation and repair. It is not necessary that such cotreatment drugs be included per se in the compositions of this invention, although this will be convenient where such drugs are proteinaceous. Such admixtures are suitably administered in the same manner and for the same purposes as the VEGF-E used alone. The useful molar ratio of VEGF-E to such secondary growth factors is typically 1:0.1-10, with about equimolar amounts being preferred.

The compounds of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the PRO polypeptide hereof is combined in admixture with a pharmaceutically acceptable carrier vehicle. Suitable carrier vehicles and their formulation, inclusive of other human proteins, e.g., human serum albumin, are described, for example, in *Remington's Pharmaceutical Sciences*, 16th ed., 1980, Mack Publishing Co., edited by Oslo *et al.* the disclosure of which is hereby incorporated by reference. The VEGF-E herein may be administered parenterally to subjects suffering from cardiovascular diseases or conditions, or by other methods that ensure its delivery to the bloodstream in an effective form.

Compositions particularly well suited for the clinical administration of VEGF-E hereof employed in the practice of the present invention include, for example, sterile aqueous solutions, or sterile hydratable powders

such as lyophilized protein. It is generally desirable to include further in the formulation an appropriate amount of a pharmaceutically acceptable salt, generally in an amount sufficient to render the formulation isotonic. A pH regulator such as arginine base, and phosphoric acid, are also typically included in sufficient quantities to maintain an appropriate pH, generally from 5.5 to 7.5. Moreover, for improvement of shelf-life or stability of aqueous formulations, it may also be desirable to include further agents such as glycerol. In this manner, variant t-PA formulations are rendered appropriate for parenteral administration, and, in particular, intravenous administration.

Dosages and desired drug concentrations of pharmaceutical compositions of the present invention may vary depending on the particular use envisioned. For example, in the treatment of deep vein thrombosis or peripheral vascular disease, "bolus" doses, will typically be preferred with subsequent administrations being given to maintain an approximately constant blood level, preferably on the order of about 3 μg/ml.

However, for use in connection with emergency medical care facilities where infusion capability is generally not available and due to the generally critical nature of the underlying disease (e.g., embolism, infarct), it will generally be desirable to provide somewhat larger initial doses, such as an intravenous bolus.

For the various therapeutic indications referred to for the compounds hereof, the VEGF-E molecules will be formulated and dosed in a fashion consistent with good medical practice taking into account the specific disorder to be treated, the condition of the individual patient, the site of delivery, the method of administration and other factors known to practitioners in the respective art. Thus, for purposes herein, the "therapeutically effective amount" of the VEGF-E molecules hereof is an amount that is effective either to prevent, lessen the worsening of, alleviate, or cure the treated condition, in particular that amount which is sufficient to enhance the survival, proliferation or differentiation of targeted cells in vivo. In general a dosage is employed capable of establishing in the tissue that is the target for the therapeutic indication being treated a level of a VEGF-E hereof greater than about 0.1 ng/cm^3 up to a maximum dose that is efficacious but not unduly toxic. It is contemplated that intra-tissue administration may be the choice for certain of the therapeutic indications for the compounds hereof.

The human Toll proteins of the present invention can also be used in assays to identify other proteins or molecules involved in Toll-mediated signal transduction. For example, PRO285 and PRO286 are useful in identifying the as of yet unknown natural ligands of human Tolls, or other factors that participate (directly or indirectly) in the activation of and/or signaling through a human Toll receptor, such as potential Toll receptor associated kinases. In addition, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Screening assays can be designed to find lead compounds that mimic the biological activity of a native Toll polypeptide or a ligand for a native Toll polypeptide. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the

art.

In vitro assays employ a mixture of components including a Toll receptor polypeptide, which may be part of fusion product with another peptide or polypeptide, e.g., a tag for detecting or anchoring, etc. The assay mixtures may further comprise (for binding assays) a natural intra- or extracellular Toll binding target (i.e. a Toll ligand, or another molecule known to activate and/or signal through the Toll receptor). While native binding targets may be used, it is frequently preferred to use portion of such native binding targets (e.g. peptides), so long as the portion provides binding affinity and avidity to the subject Toll protein conveniently measurable in the assay. The assay mixture also contains a candidate pharmacological agent. Candidate agents encompass numerous chemical classes, through typically they are organic compounds, preferably small organic compounds, and are obtained from a wide variety of sources, including libraries of synthetic or natural compounds. A variety of other reagents may also be included in the mixture, such as, salts, buffers, neutral proteins, e.g. albumin, detergents, protease inhibitors, nuclease inhibitors, antimicrobial agents, etc.

In *in vitro* binding assays, the resultant mixture is incubated under conditions whereby, but for the presence of the candidate molecule, the Toll protein specifically binds the cellular binding target, portion or analog, with a reference binding affinity. The mixture components can be added in any order that provides for the requisite bindings and incubations may be performed at any temperature which facilitates optimal binding. Incubation periods are likewise selected for optimal binding but also minimized to facilitate rapid high-throughput screening.

After incubation, the agent-biased binding between the Toll protein and one or more binding targets is detected by any convenient technique. For cell-free binding type assays, a separation step is often used to separate bound from unbound components. Separation may be effected by precipitation (e.g. TCA precipitation, immunoprecipitation, etc.), immobilization (e.g on a solid substrate), etc., followed by washing by, for example, membrane filtration (e.g. Whatman's P-18 ion exchange paper, Polyfiltronic's hydrophobic GFC membrane, etc.), gel chromatography (e.g. gel filtration, affinity, etc.). For Toll-dependent transcription assays, binding is detected by a change in the expression of a Toll-dependent reporter.

Detection may be effected in any convenient way. For cell-free binding assays, one of the components usually comprises or is coupled to a label. The label may provide for direct detection as radioactivity, luminescence, optical or electron density, etc., or indirect detection, such as, an epitope tag, an enzyme, etc. A variety of methods may be used to detect the label depending on the nature of the label and other assay components, e.g. through optical or electron density, radiative emissions, nonradiative energy transfers, etc. or indirectly detected with antibody conjugates, etc.

Nucleic acid encoding the Toll polypeptides disclosed herein may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve *in vivo* synthesis of a therapeutically effective genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain

genes *in vivo*. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane. (Zamecnik *et al.*, Proc. Natl. Acad. Sci. USA 83, 4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred *in vivo* gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau *et al.*, Trends in Biotechnology 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu *et al.*, J. Biol. Chem. 262, 4429-4432 (1987); and Wagner *et al.*, Proc. Natl. Acad. Sci. USA 87, 3410-3414 (1990). For review of the currently known gene marking and gene therapy protocols see Anderson *et al.*, Science 256, 808-813 (1992).

The various uses listed in connection with the Toll proteins herein, are also available for agonists of the native Toll receptors, which mimic at least one biological function of a native Toll receptor.

Neurotrimin as well as other members of the IgLON subfamily of the immunoglobulin superfamily have been identified to have effect upon neural patterning, differentiation, maturation and growth. As a result, PRO337 the human neurotrimin homolog polypeptides would be expected to have utility in diseases which are characterized by neural disfunction. For example, motoneuron disorders such as amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and various conditions involving spinal muscular atrophy, or paralysis. NGF variant formulations of the invention can be used to treat human neurodegenerative disorders, such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's Syndrome, nerve deafness, and Meniere's disease. Moreover PRO337 polypeptide may also be used as a cognitive enhancer, to enhance learning particularly in dementia or trauma, such as those associated with the above diseases.

Further, PRO337 may be employed to treat neuropathy, and especially peripheral neuropathy. "Peripheral neuropathy" refers to a disorder affecting the peripheral nervous system, most often manifested as one or a combination of motor, sensory, sensorimotor, or autonomic neural dysfunction. The wide variety of morphologies exhibited by peripheral neuropathies can each be attributed uniquely to an equally wide number of causes. For example, peripheral neuropathies can be genetically acquired, can result from a systemic disease,

or can be induced by a toxic agent. Examples include but are not limited to diabetic peripheral neuropathy, distal sensorimotor neuropathy, or autonomic neuropathies such as reduced motility of the gastrointestinal tract or atony of the urinary bladder. Examples of neuropathies associated with systemic disease include post-polio syndrome or AIDS-associated neuropathy; examples of hereditary neuropathies include Charcot-Marie-Tooth disease, Refsum's disease, Abetalipoproteinemia, Tangier disease, Krabbe's disease, Metachromatic leukodystrophy, Fabry's disease, and Dejerine-Sottas syndrome; and examples of neuropathies caused by a toxic agent include those caused by treatment with a chemotherapeutic agent such as vincristine, cisplatin, methotrexate, or 3'-azido-3'-deoxythymidine. Correspondingly, neurotrimin antagonists would be expected to have utility in diseases characterized by excessive neuronal activity.

Endothelin is generated from inactive intermediates, the big endothelins, by a unique processing event catalyzed by the zinc metalloprotease, endothelin converting enzyme (ECE). ECE was recently cloned, and its structure was shown to be a single pass transmembrane protein with a short intracellular N-terminal and a long extracellular C-terminal that contains the catalytic domain and numerous N-glycosylation sites. ECEs cleave the endothelin propeptide between Trp73 and Val74 producing the active peptide, ET, which appears to function as a local rather than a circulating hormone (Rubanyi, G.M. & Polokoff, M.A., Pharmacological Reviews 46: 325-415 (1994). Thus ECE activity is a potential site of regulation of endothelin production and a possible target for therapeutic intervention in the endothelin system. By blocking ECE activity, it is possible stop the production of ET-1 by inhibiting the conversion of the relatively inactive precursor, big ET-1, to the physiologically active form.

ECE-2 is 64% identical to bovine ECE-2 at the amino acid level. ECE-2 is closely related to ECE-1 (63% identical, 80% conserved), neutral endopeptidase 24.11 and the Kell blood group protein. Bovine ECE-2 is a type II membrane-bound metalloproteinase localized in the trans-Golgi network where it acts as an intracellular enzyme converting endogenous big endothelin-1 into active endothelin (Emoto, N. and Yanangisawa, M., J. Biol. Chem. 270: 15262-15268 (1995). The bovine ECE-2 mRNA expression is highest in parts of the brain, cerebral cortex, cerebellum and adrenal medulla. It is expressed at lower levels in mymetrium, testes, ovary, and endothelial cells. Bovine ECE-2 and ECE-1 both are more active on ET-1 as a substrate compared to ET-2 or ET-3, Emoto and Yanangisawa, supra.

Human ECE-2 is 736 amino acids in length with a 31 residue amino-terminal tail, a 23 residue transmembrane helix and a 682 carboxy-terminal domain. It is 94% identical to bovine ECE-2 and 64% identical to human ECE-1. The predicted transmembrane domain is highly conserved between the human and bovine ECE-2 proteins and between human ECE-1 and human ECE-2, as are the putative N-linked glycosylation sites, Cys residues conserved in the neutral endopeptidase 24.11 and the Kell blood group protein family and the putative zinc binding motif. The sequence suggests, that like other members of the NEP-ECE-Kell family, human ECE-2 encodes a type II transmembrane zinc-binding metalloproteinase, which, by extrapolation from what is known about bovine ECE-2, is an intracellular enzyme located within the secretory pathway which processes endogenously produced big ET-1 while it is still in the secretory vesicles. Emoto and Yanangisawa, supra.

The expression pattern of ECE-2 differs from that observed for ECE-1. Northern blot analysis of

mRNA levels indicated low levels of expression of a 3.3 kb transcript in adult brain (highest in the cerebellum, putamen, medulla and temporal lobe, and lower in the cerebral cortex, occipital lobe and frontal lobe), spinal cord, lung and pancreas and higher levels of a 4.5 kb transcript in fetal brain and kidney. The two transcript sizes probably represent the use of alternative polyadenylation sites as has been observed for bovine ECE-2 (Emoto and Yanangisawa, supra) and ECE-1 (Xu et al., Cell 78: 473-485 (1994). PCR on cDNA libraries indicated low levels of expression in fetal brain, fetal kidney, fetal small intestine and adult testis. Fetal liver, fetal lung and adult pancreas were all negative.

The endothelin (ET) family of peptides have potent vascular, cardiac and renal actions which may be of pathophysiological importance in many human disease states. ET-1 is expressed as an inactive 212 amino acid prepropeptide. The prepropeptide is first cleaved at Arg52-Cys53 and Arg92-Ala93 and then the carboxy terminal Lys91 and Arg92 are trimmed from the protein to generate the propeptide big ET-1. ECEs then cleave the propeptide between Trp73 and Val74, producing the active peptide, ET, which appears to function as a local rather than a circulating hormone (Rubanyi and Polokoff, Pharma. R. 46: 325-415 (1994).

Endothelins may play roles in the pathophysiology of a number of disease states including: 1) cardiovascular diseases (vasospasm, hypertension, myocardial ischemia; reperfusion injury and acute myochardial infarction, stroke (cerebral ischemia), congestive heart failure, shock, atherosclerosis, vascular thickening); 2) kidney disease (acute and chronic renal failure, glomerulonephritis, cirrhosis); 3) lung disease (bronchial asthma, pulmonary hypertension); 4) gastrointestinal disorders (gastric ulcer, inflammatory bowel diseases); 5) reproductive disorders (premature labor, dysmenorhea, preeclampsia) and 6) carcinogenesis. Rubanyi & Polokoff, supra.

Diseases can be evaluated for the impact of ET upon them by examining: 1) increased production of ETs; 2) increased reactivity to ETs; and/or 3) efficacy of an ET receptor antagonist, antibody or ECE inhibitor. Response to the previous criteria suggest that ETs likely play roles in cerebral vasospasm following subarachnoid hemorrhage, hypertension (fulminant/complications), acute renal failure and congestive heart failure. While inhibitors of ET production or activity have not been used in models of coronary vasospasm, acute myocardial infarction, and atherosclerosis, they do have elevated ET levels and increase reactivity to ETs. Shock and pulmonary hypertension also exhibit elevated ET levels (Rubanyi and Polokoff, supra). Inhibition of ECEs in these conditions may be of therapeutic value.

The expression pattern of ECE-2 differs from that observed for ECE-1. ECE-2 was observed at low levels in the adult brain, lung and pancreas and higher levels in fetal brain and kidney by Northern blot analysis (Fig. 8). PCR revealed low levels of expression in additional tissues: fetal lung, fetal small intestine and adult testis. Fetal liver was negative. A similar pattern was reported for bovine ECE-2 (Emoto and Yanangisawa, supra). It is expressed in brain tissues (cerebral cortex, cerebellum and adrenal medulla), myometrium and testis, and in low levels in ovary and very low levels in many other tissues. Bovine ECE-1 (Xu et al, supra) is more widely and more abundantly expressed. It is observed in vascular endothelial cells of most organs and in some parenchymal cells. With the exception for brain, bovine ECE-2 mRNA was present at lower levels than ECE-1. Applicants believe ECE-2 to be a particularly good target for the therapeutic intervention for diseases

such as cerebral vasospasm following subarachnoid hemorrhage and stroke.

92. Anti-PRO Polypeptide Antibodies

The present invention further provides anti-PRO polypeptide antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

A. Polyclonal Antibodies

The anti-PRO polypeptide antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

B. Monoclonal Antibodies

The anti-PRO polypeptide antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the PRO polypeptide of interest or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Rockville, Maryland. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, *J. Immunol.*, 133:3001 (1984); Brodeur *et al., Monoclonal Antibody Production Techniques and Applications*, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the PRO polypeptide of interest. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, *Anal. Biochem.*, 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, supra]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., supra] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent

heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

C. Humanized Antibodies

The anti-PRO polypeptide antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones *et al., Nature*, 321: 522-525 (1986); Riechmann *et al., Nature*, 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones *et al., Nature*, 321: 522-525 (1986); Riechmann *et al., Nature*, 332:323-327 (1988); Verhoeyen *et al., Science*, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks *et al., J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole *et al.* and Boerner *et al.* are also available for the preparation of human

monoclonal antibodies (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner *et al.*, *J. Immunol.*, 147(1):86-95 (1991)].

D. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO polypeptide, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, *Nature*, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, *EMBO J.*, 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, *Methods in Enzymology*, 121:210 (1986).

E. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

93. Uses for Anti-PRO Polypeptide Antibodies

The anti-PRO polypeptide antibodies of the invention have various utilities. For example, anti-PRO

polypeptide antibodies may be used in diagnostic assays for a PRO polypeptide, *e.g.*, detecting its expression in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, Monoclonal Antibodies: A Manual of Techniques, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as ^{3}H, ^{14}C, ^{32}P, ^{35}S, or ^{125}I, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter *et al.*, *Nature*, 144:945 (1962); David *et al.*, *Biochemistry*, 13:1014 (1974); Pain *et al.*, *J. Immunol. Meth.*, 40:219 (1981); and Nygren, *J. Histochem. and Cytochem.*, 30:407 (1982).

Anti-PRO polypeptide antibodies also are useful for the affinity purification of PRO polypeptide from recombinant cell culture or natural sources. In this process, the antibodies against the PRO polypeptide are immobilized on a suitable support, such a Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the PRO polypeptide to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the PRO polypeptide, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the PRO polypeptide from the antibody.

Anti-Toll receptor (i.e., anti-PRO285 and anti-PRO286 antibodies) may also be useful in blocking the biological activities of the respective Toll receptors. The primary function of the family of Toll receptors is believed to be to act as pathogen pattern recognition receptors sensing the presence of conserved molecular pattern present on microbes. Lipopolysaccharides (LPS, also known as endotoxins), potentially lethal molecules produced by various bacteria, bind to the lipopolysaccharide binding protein (LBP) in the blood. The complex formed then activates a receptor known as CD14. There is no consensus in the art about what happens next. According to a hypothesis, CD14 does not directly instruct macrophages to produce cytokines, cell adhesion proteins and enzymes involved in the production of lower molecular weight proinflammatory mediators, rather enables LPS to activate a second receptor. Alternatively, it has been suggested that LPS may activate certain receptors directly, without help from LBP or CD14. The data disclosed in the present application indicate that the human toll-like receptors are signaling receptors that are activated by LPS in an LBP and CD14 responsive manner. As this mechanism, under pathophysiologic conditions can lead to an often fatal syndrome called septic shock; anti-Toll receptor antibodies (just as other Toll receptor antagonists) might be useful in the treatment of septic shock. It is foreseen that the different Toll receptors might recognize different pathogens, e.g., various strains of Gram-negative or Gram-positive bacteria. Accordingly, in certain situations, combination therapy with a mixture of antibodies specifically binding different Toll receptors, or the use of bispecific anti-Toll antibodies may be desirable.

It is specifically demonstrated that anti-huTLR2 antibodies are believed to be specifically useful in

blocking the induction of this receptor by LPS. As it has been shown that LPS exposure can lead to septic shock (Parrillo, N. Engl. J. Med. 328, 1471-1477 [1993]), anti-huTLR2 antibodies are potentially useful in the treatment of septic shock.

The foregoing therapeutic and diagnostic uses listed in connection with the anti-Toll receptor antibodies are also applicable to other Toll antagonists, i.e., other molecules (proteins, peptides, small organic molecules, etc.) that block Toll receptor activation and/or signal transduction mediated by Toll receptors.

In view of their therapeutic potentials, the Toll proteins (including variants of the native Toll homologues), and their agonists and antagonists (including but not limited to anti-Toll antibodies) are incorporated in compositions suitable for therapeutic use. Therapeutic compositions are prepared for storage by mixing the active ingredient having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th Edition, Osol, A. Ed. 1980) in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as Tween, Pluronics or PEG.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacylate) microcapsules, respectively), in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, *supra*.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

The route of administration is in accord with known methods, e.g. injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial or intralesional routes, topical administration, or by sustained release systems.

Suitable examples of sustained release preparations include semipermeable polymer matrices in the form of shaped articles, e.g. films, or microcapsules. Sustained release matrices include polyesters, hydrogels, polylactides (U.S. Patent 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (U. Sidman *et al.*, Biopolymers 22 (1): 547-556 [1983]), poly (2-hydroxyethyl-methacrylate) (R. Langer, et al., J. Biomed. Mater. Res. 15: 167-277 [1981] and R. Langer, Chem. Tech. 12: 98-105 [1982]), ethylene vinyl acetate (R. Langer et al., Id.) or poly-D-(-)-3-hydroxybutyric acid (EP 133,988). Sustained release compositions

also include liposomes. Liposomes containing a molecule within the scope of the present invention are prepared by methods known per se: DE 3,218,121; Epstein *et al.*, Proc. Natl. Acad. Sci. USA 82: 3688-3692 (1985); Hwang *et al.*, Proc. Natl. Acad. Sci. USA 77: 4030-4034 (1980); EP 52322; EP 36676A; EP 88046; EP 143949; EP 142641; Japanese patent application 83-118008; U.S. patents 4,485,045 and 4,544,545; and EP 102,324. Ordinarily the liposomes are of the small (about 200-800 Angstroms) unilamelar type in which the lipid content is greater than about 30 mol. % cholesterol, the selected proportion being adjusted for the optimal NT-4 therapy.

An effective amount of the active ingredient will depend, for example, upon the therapeutic objectives, the route of administration, and the condition of the patient. Accordingly, it will be necessary for the therapist to titer the dosage and modify the route of administration as required to obtain the optimal therapeutic effect. A typical daily dosage might range from about 1 μg/kg to up to 100 mg/kg or more, depending on the factors mentioned above. Typically, the clinician will administer a molecule of the present invention until a dosage is reached that provides the required biological effect. The progress of this therapy is easily monitored by conventional assays.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Rockville, Maryland.

EXAMPLE 1: Extracellular Domain Homology Screening to Identify Novel Polypeptides and cDNA Encoding Therefor

The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST databases included public databases (e.g., Dayhoff, GenBank), and proprietary databases (e.g. LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or BLAST2 (Altschul and Gish, Methods in Enzymology 266: 460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a Blast score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, WA; (http://bozeman.mbt.washington.edu/phrap.docs/phrap.html).

Using this extracellular domain homology screen, consensus DNA sequences were assembled relative

to the other identified EST sequences using phrap. In addition, the consensus DNA sequences obtained were often (but not always) extended using repeated cycles of BLAST and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above.

Based upon the consensus sequences obtained as described above, oligonucleotides were then synthesized and used to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for a PRO polypeptide. Forward (.f) and reverse (.r) PCR primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe (.p) sequences are typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel et al., Current Protocols in Molecular Biology, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

EXAMPLE 2: Isolation of cDNA clones by Amylase Screening

1. Preparation of oligo dT primed cDNA library

mRNA was isolated from a human tissue of interest using reagents and protocols from Invitrogen, San Diego, CA (Fast Track 2). This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, MD (Super Script Plasmid System). In this procedure, the double stranded cDNA was sized to greater than 1000 bp and the SalI/NotI linkered cDNA was cloned into XhoI/NotI cleaved vector. pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites.

2. Preparation of random primed cDNA library

A secondary cDNA library was generated in order to preferentially represent the 5' ends of the primary cDNA clones. Sp6 RNA was generated from the primary library (described above), and this RNA was used to generate a random primed cDNA library in the vector pSST-AMY.0 using reagents and protocols from Life Technologies (Super Script Plasmid System, referenced above). In this procedure the double stranded cDNA was sized to 500-1000 bp, linkered with blunt to NotI adaptors, cleaved with SfiI, and cloned into SfiI/NotI cleaved vector. pSST-AMY.0 is a cloning vector that has a yeast alcohol dehydrogenase promoter preceding the cDNA cloning sites and the mouse amylase sequence (the mature sequence without the secretion signal)

followed by the yeast alcohol dehydrogenase terminator, after the cloning sites. Thus, cDNAs cloned into this vector that are fused in frame with amylase sequence will lead to the secretion of amylase from appropriately transfected yeast colonies.

3. Transformation and Detection

DNA from the library described in paragraph 2 above was chilled on ice to which was added electrocompetent DH10B bacteria (Life Technologies, 20 ml). The bacteria and vector mixture was then electroporated as recommended by the manufacturer. Subsequently, SOC media (Life Technologies, 1 ml) was added and the mixture was incubated at 37°C for 30 minutes. The transformants were then plated onto 20 standard 150 mm LB plates containing ampicillin and incubated for 16 hours (37°C). Positive colonies were scraped off the plates and the DNA was isolated from the bacterial pellet using standard protocols, e.g. CsCl-gradient. The purified DNA was then carried on to the yeast protocols below.

The yeast methods were divided into three categories: (1) Transformation of yeast with the plasmid/cDNA combined vector; (2) Detection and isolation of yeast clones secreting amylase; and (3) PCR amplification of the insert directly from the yeast colony and purification of the DNA for sequencing and further analysis.

The yeast strain used was HD56-5A (ATCC-90785). This strain has the following genotype: MAT alpha, ura3-52, leu2-3, leu2-112, his3-11, his3-15, MAL^+, SUC^+, GAL^+. Preferably, yeast mutants can be employed that have deficient post-translational pathways. Such mutants may have translocation deficient alleles in *sec71*, *sec72*, *sec62*, with truncated *sec71* being most preferred. Alternatively, antagonists (including antisense nucleotides and/or ligands) which interfere with the normal operation of these genes, other proteins implicated in this post translation pathway (e.g., SEC61p, SEC72p, SEC62p, SEC63p, TDJ1p or SSA1p-4p) or the complex formation of these proteins may also be preferably employed in combination with the amylase-expressing yeast.

Transformation was performed based on the protocol outlined by Gietz et al., Nucl. Acid. Res., 20:1425 (1992). Transformed cells were then inoculated from agar into YEPD complex media broth (100 ml) and grown overnight at 30°C. The YEPD broth was prepared as described in Kaiser et al., Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 207 (1994). The overnight culture was then diluted to about 2 x 10^6 cells/ml (approx. OD_{600}=0.1) into fresh YEPD broth (500 ml) and regrown to 1 x 10^7 cells/ml (approx. OD_{600}=0.4-0.5).

The cells were then harvested and prepared for transformation by transfer into GS3 rotor bottles in a Sorval GS3 rotor at 5,000 rpm for 5 minutes, the supernatant discarded, and then resuspended into sterile water, and centrifuged again in 50 ml falcon tubes at 3,500 rpm in a Beckman GS-6KR centrifuge. The supernatant was discarded and the cells were subsequently washed with LiAc/TE (10 ml, 10 mM Tris-HCl, 1 mM EDTA pH 7.5, 100 mM Li_2OOCCH_3), and resuspended into LiAc/TE (2.5 ml).

Transformation took place by mixing the prepared cells (100 μl) with freshly denatured single stranded salmon testes DNA (Lofstrand Labs, Gaithersburg, MD) and transforming DNA (1 μg, vol. < 10 μl) in

microfuge tubes. The mixture was mixed briefly by vortexing, then 40% PEG/TE (600 μl, 40% polyethylene glycol-4000, 10 mM Tris-HCl, 1 mM EDTA, 100 mM Li_2OOCCH_3, pH 7.5) was added. This mixture was gently mixed and incubated at 30°C while agitating for 30 minutes. The cells were then heat shocked at 42°C for 15 minutes, and the reaction vessel centrifuged in a microfuge at 12,000 rpm for 5-10 seconds, decanted and resuspended into TE (500 μl, 10 mM Tris-HCl, 1 mM EDTA pH 7.5) followed by recentrifugation. The cells were then diluted into TE (1 ml) and aliquots (200 μl) were spread onto the selective media previously prepared in 150 mm growth plates (VWR).

Alternatively, instead of multiple small reactions, the transformation was performed using a single, large scale reaction, wherein reagent amounts were scaled up accordingly.

The selective media used was a synthetic complete dextrose agar lacking uracil (SCD-Ura) prepared as described in Kaiser et al., Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 208-210 (1994). Transformants were grown at 30°C for 2-3 days.

The detection of colonies secreting amylase was performed by including red starch in the selective growth media. Starch was coupled to the red dye (Reactive Red-120, Sigma) as per the procedure described by Biely et al., Anal. Biochem., 172:176-179 (1988). The coupled starch was incorporated into the SCD-Ura agar plates at a final concentration of 0.15% (w/v), and was buffered with potassium phosphate to a pH of 7.0 (50-100 mM final concentration).

The positive colonies were picked and streaked across fresh selective media (onto 150 mm plates) in order to obtain well isolated and identifiable single colonies. Well isolated single colonies positive for amylase secretion were detected by direct incorporation of red starch into buffered SCD-Ura agar. Positive colonies were determined by their ability to break down starch resulting in a clear halo around the positive colony visualized directly.

4. Isolation of DNA by PCR Amplification

When a positive colony was isolated, a portion of it was picked by a toothpick and diluted into sterile water (30 μl) in a 96 well plate. At this time, the positive colonies were either frozen and stored for subsequent analysis or immediately amplified. An aliquot of cells (5 μl) was used as a template for the PCR reaction in a 25 μl volume containing: 0.5 μl Klentaq (Clontech, Palo Alto, CA); 4.0 μl 10 mM dNTP's (Perkin Elmer-Cetus); 2.5 μl Kentaq buffer (Clontech); 0.25 μl forward oligo 1; 0.25 μl reverse oligo 2; 12.5 μl distilled water. The sequence of the forward oligonucleotide 1 was:

5'-TGTAAAACGACGGCCAGTTAAATAGACCTGCAATTATTAATCT-3' (SEQ ID NO:324)

The sequence of reverse oligonucleotide 2 was:

5'-CAGGAAACAGCTATGACCACCTGCACACCTGCAAATCCATT-3' (SEQ ID NO:325)

PCR was then performed as follows:

a.		Denature	92°C, 5 minutes
b.	3 cycles of:	Denature	92°C, 30 seconds
		Anneal	59°C, 30 seconds

		Extend	72°C,	60 seconds
c.	3 cycles of:	Denature	92°C,	30 seconds
		Anneal	57°C,	30 seconds
		Extend	72°C,	60 seconds
d.	25 cycles of:	Denature	92°C,	30 seconds
		Anneal	55°C,	30 seconds
		Extend	72°C,	60 seconds
e.		Hold	4°C	

The underlined regions of the oligonucleotides annealed to the ADH promoter region and the amylase region, respectively, and amplified a 307 bp region from vector pSST-AMY.0 when no insert was present. Typically, the first 18 nucleotides of the 5' end of these oligonucleotides contained annealing sites for the sequencing primers. Thus, the total product of the PCR reaction from an empty vector was 343 bp. However, signal sequence-fused cDNA resulted in considerably longer nucleotide sequences.

Following the PCR, an aliquot of the reaction (5 μl) was examined by agarose gel electrophoresis in a 1% agarose gel using a Tris-Borate-EDTA (TBE) buffering system as described by Sambrook et al., supra. Clones resulting in a single strong PCR product larger than 400 bp were further analyzed by DNA sequencing after purification with a 96 Qiaquick PCR clean-up column (Qiagen Inc., Chatsworth, CA).

EXAMPLE 3: Isolation of cDNA Clones Encoding Human PRO213

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA28735. Based on the DNA28735 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO213.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-TGGAGCAGCAATATGCCAGCC-3' (SEQ ID NO:3)

reverse PCR primer 5'-TTTTCCACTCCTGTCGGGTTGG-3' (SEQ ID NO:4)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA28735 sequence which had the following nucleotide sequence

hybridization probe

5'-GGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGG-3' (SEQ ID NO:5)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO213 gene using the probe oligonucleotide and one of the PCR primers. RNA

for construction of the cDNA libraries was isolated from human fetal lung tissue.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO213 [herein designated as UNQ187 (DNA30943-1163)] (SEQ ID NO:1) and the derived protein sequence for PRO213.

The entire nucleotide sequence of UNQ187 (DNA30943-1163) is shown in Figure 1 (SEQ ID NO:1). Clone UNQ187 (DNA30943-1163) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 336-338 and ending at the stop codon at nucleotide positions 1221-1223 (Figure 1). The predicted polypeptide precursor is 295 amino acids long (Figure 2). Clone UNQ187 (DNA30943-1163) has been deposited with ATCC.

Analysis of the amino acid sequence of the full-length PRO213 polypeptide suggests that a portion of it possesses significant homology to the human growth arrest-specific gene 6 protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO213 amino acid sequence and the following Dayhoff sequences, HSMHC3W5A_6 and B48089.

EXAMPLE 4: Isolation of cDNA Clones Encoding Human PRO274

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA36469. Based on the DNA36469 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO274. ESTs proprietary to Genentech were employed in the consensus assembly. The ESTs are shown in Figures 5-7 and are herein designated DNA17873, DNA36157 and DNA28929, respectively.

Pairs of PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 (36469.f1) 5'-CTGATCCGGTTCTTGGTGCCCCTG-3' (SEQ ID NO:11)
forward PCR primer 2 (36469.f2) 5'-GCTCTGTCACTCACGCTC-3' (SEQ ID NO:12)
forward PCR primer 3 (36469.f3) 5'-TCATCTCTTCCCTCTCCC-3' (SEQ ID NO:13)
forward PCR primer 4 (36469.f4) 5'-CCTTCCGCCACGGAGTTC-3' (SEQ ID NO:14)
reverse PCR primer 1 (36469.r1) 5'-GGCAAAGTCCACTCCGATGATGTC-3' (SEQ ID NO:15)
reverse PCR primer 2 (36469.r2) 5'-GCCTGCTGTGGTCACAGGTCTCCG-3' (SEQ ID NO:16)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA36469 sequence which had the following nucleotide sequence

hybridization probe (36469.p1)
5'-TCGGGGAGCAGGCCTTGAACCGGGGCATTGCTGCTGTCAAGGAGG-3' (SEQ ID NO:17)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO274 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal liver tissue (LIB229).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for

PRO274 [herein designated as UNQ241 (DNA39987-1184)] (SEQ ID NO:1) and the derived protein sequence for PRO274.

The entire nucleotide sequence of UNQ241 (DNA39987-1184) is shown in Figure 3 (SEQ ID NO:6). Clone UNQ241 (DNA39987-1184) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 83-85 and ending at the stop codon at nucleotide positions 1559-1561 (Figure 3). The predicted polypeptide precursor is 492 amino acids long (Figure 4), has an estimated molecular weight of about 54,241 daltons and an estimated pI of about 8.21. Clone UNQ241 (DNA39987-1184) has been deposited with ATCC and is assigned ATCC deposit no. 209786.

Analysis of the amino acid sequence of the full-length PRO274 polypeptide suggests that it possesses significant homology to the Fn54 protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO274 amino acid sequence and the following Dayhoff sequences, MMFN54S2_1, MMFN54S1_1, CELF48C1_8, CEF38B7_6, PRP3_RAT, INL3_PIG, MTCY07A7_13, YNAX_KLEAE, A47234 and HME2_MOUSE.

EXAMPLE 5: Isolation of cDNA Clones Encoding Human PRO300

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA35930. Based on the DNA35930 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO300.

Forward and reverse PCR primers were synthesized:

forward PCR primer 1 (35930.f1) 5'-GCCGCCTCATCTTCACGTTCTTCC-3' (SEQ ID NO:20)
forward PCR primer 2 (35930.f2) 5'-TCATCCAGCTGGTGCTGCTC-3' (SEQ ID NO:21)
forward PCR primer 3 (35930.f3) 5'-CTTCTTCCACTTCTGCCTGG-3' (SEQ ID NO:22)
forward PCR primer 4 (35930.f4) 5'-CCTGGGCAAAAATGCAAC-3' (SEQ ID NO:23)
reverse PCR primer 1 (35930.r1) 5'-CAGGAATGTAGAAGGCACCCACGG-3' (SEQ ID NO:24)
reverse PCR primer 2 (35930.r2) 5'-TGGCACAGATCTTCACCCACACGG-3' (SEQ ID NO:25)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35930 sequence which had the following nucleotide sequence

hybridization probe (35930.p1)
5'-TGTCCATCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG-3' (SEQ ID NO:26)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO300 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO300 [herein designated as UNQ263 (DNA40625-1189)] (SEQ ID NO:18) and the derived protein sequence

for PRO300.

The entire nucleotide sequence of UNQ263 (DNA40625-1189) is shown in Figure 8 (SEQ ID NO:18). Clone UNQ263 (DNA40625-1189) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 45-47 and ending at the stop codon at nucleotide positions 1416-1418 (Figure 8). The predicted polypeptide precursor is 457 amino acids long (Figure 9). Clone UNQ263 (DNA40625-1189) has been deposited with ATCC and is assigned ATCC deposit no. 209788.

Analysis of the amino acid sequence of the full-length PRO300 polypeptide suggests that portions of it possess significant homology to the Diff 33 protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO300 amino acid sequence and the following Dayhoff sequence, HSU49188_1.

EXAMPLE 6: Isolation of cDNA Clones Encoding Human PRO284

Two cDNA sequences were isolated in the amylase screen described in Example 2 and those cDNA sequences are herein designated DNA12982 (see Figure 12; human placenta-derived) and DNA15886 (see Figure 13; human salivary gland-derived). The DNA12982 and DNA15886 sequences were then clustered and aligned, giving rise to a consensus nucleotide sequence herein designated DNA18832.

Based on the DNA18832 consensus sequence, oligonucleotide probes were generated and used to screen a human placenta library (LIB89) prepared as described in paragraph 1 of Example 2 above. The cloning vector was pRK5B (pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)), and the cDNA size cut was less than 2800 bp.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 (18832.est.f) 5'-TCGTACAGTTACGCTCTCCC-3' (SEQ ID NO:31)

forward PCR primer 2 (18832.f) 5'-CTTGAGGAGCGTCAGAAGCG-3' (SEQ ID NO:32)

reverse PCR primer (18832.r) 5'-ATAACGAATGAAGCCTCGTG-3' (SEQ ID NO:33)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA18832 sequence which had the following nucleotide sequence

hybridization probe (18832.p)

5'-GCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTG-3' (SEQ ID NO:34)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO284 gene using the probe oligonucleotide and one of the PCR primers.

A full length clone was identified that contained a single open reading frame with an apparent translational initiation site at nucleotide positions 167-169 and ending at the stop codon found at nucleotide positions 1022-1024 (Figure 10; SEQ ID NO:27). The predicted polypeptide precursor is 285 amino acids long, has a calculated molecular weight of approximately 32,190 daltons and an estimated pI of approximately 9.03. Analysis of the full-length PRO284 sequence shown in Figure 11 (SEQ ID NO:28) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 24, transmembrane domains from

about amino acid 76 to about amino acid 96 and from about amino acid 171 to about amino acid 195 and a potential N-glycosylation site from about amino acid 153 to about amino acid 156. Clone UNQ247 (DNA23318-1211) has been deposited with ATCC on April 21, 1998 and is assigned ATCC deposit no. 209787.

Analysis of the amino acid sequence of the full-length PRO284 polypeptide suggests that it possesses no significant sequence similarity to any known protein. However, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced some degree of homology between the PRO284 amino acid sequence and the following Dayhoff sequences, JQ0124, CELE04A4_5, AB006451_1, AF030162_1, IM23_YEAST, S71194, NIA_CUCMA, IM17_YEAST, I50479 and HUMZFHP_1.

EXAMPLE 7: Isolation of cDNA Clones Encoding Human PRO296

A cDNA sequence isolated in the amylase screen as described in Example 2 above was found, by BLAST and FastA sequence alignment, to have sequence homology to a nucleotide sequence encoding sarcoma-associated protein SAS. This cDNA sequence is herein designated DNA23020 (see Figure 16). The DNA23020 sequence was then compared to a variety of expressed sequence tag (EST) databases which included public EST databases (e.g., GenBank) and a proprietary EST DNA database (LIFESEQ ™, Incyte Pharmaceuticals, Palo Alto, CA) to identify existing homologies. The homology search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into a consensus DNA sequence with the program "phrap" (Phil Green, University of Washington, Seattle, Washington; http://bozeman.mbt.washington.edu/phrap.docs/phrap.html). The consensus sequence obtained therefrom is herein designated DNA35858. Two proprietary Genentech ESTs were employed in the assembly wherein those EST sequences are herein identified as DNA21971 (Figure 17; SEQ ID NO:38) and DNA29037 (Figure 18; SEQ ID NO:39).

Based on the DNA35858 consensus sequence, oligonucleotide probes were generated and used to screen a human kidney library (LIB228) library prepared as described in paragraph 1 of Example 2 above. The cloning vector was pRK5B (pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)), and the cDNA size cut was less than 2800 bp.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 (35858.f1) 5'-ACCCACGTCTGCGTTGCTGCC-3' (SEQ ID NO:40)

forward PCR primer 2 (35858.f2) 5'-GAGAATATGCTGGAGAGG-3' (SEQ ID NO:41)

reverse PCR primer (35858.r1) 5'-AGGAATGCACTAGGATTCGCGCGG-3' (SEQ ID NO:42)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35858 sequence which had the following nucleotide sequence

hybridization probe (35858.p1)

5'-GGCCCCAAAGGCAAGGACAAAGCAGCTGTCAGGGAACCTCCGCCG-3' (SEQ ID NO:43)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to

isolate clones encoding the PRO296 gene using the probe oligonucleotide and one of the PCR primers.

A full length clone was identified that contained a single open reading frame with an apparent translational initiation site at nucleotide positions 174-176 and ending at the stop codon found at nucleotide positions 786-788 (Figure 14; SEQ ID NO:35). The predicted polypeptide precursor is 204 amino acids long, has a calculated molecular weight of approximately 22,147 daltons and an estimated pI of approximately 8.37. Analysis of the full-length PRO296 sequence shown in Figure 15 (SEQ ID NO:36) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 34 and transmembrane domains from about amino acid 47 to about amino acid 63, from about amino acid 72 to about amino acid 95 and from about amino acid 162 to about amino acid 182. Clone UNQ260 (DNA39979-1213) has been deposited with ATCC on April 21, 1998 and is assigned ATCC deposit no. 209789.

Analysis of the amino acid sequence of the full-length PRO296 polypeptide suggests that it possesses significant sequence similarity to the sarcoma-amplified SAS protein, thereby indicating that PRO296 may be a novel SAS homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO296 amino acid sequence and the following Dayhoff sequences, I58391, GEN11061, SSC2B04_1, HSU81031_2, CD63_RAT, CD63_MOUSE, CD63_HUMAN, AF022813_1, CD63_RABIT and CO02_HUMAN.

EXAMPLE 8: Isolation of cDNA Clones Encoding Human PRO329

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA35612. Based on the DNA35612 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO329.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 (35612.f1) 5'-TGGGCTGTGTCCTCATGG-3' (SEQ ID NO:46)

forward PCR primer 2 (35612.f2) 5'-TTTCCAGCGCCAATTCTC-3' (SEQ ID NO:47)

reverse PCR primer 1 (35612.r1) 5'-AGTTCTTGGACTGTGATAGCCAC-3' (SEQ ID NO:48)

reverse PCR primer 2 (35612.r2) 5'-AAACTTGGTTGTCCTCAGTGGCTG-3' (SEQ ID NO:49)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35612 sequence which had the following nucleotide sequence

hybridization probe (35612.p1)

5'-GTGAGGGACCTGTCTGCACTGAGGAGAGCAGCTGCCACACGGAGG-3' (SEQ ID NO:50)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO329 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal liver tissue (LIB6).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for

PRO329 [herein designated as UNQ291 (DNA40594-1233)] (SEQ ID NO:44) and the derived protein sequence for PRO329.

The entire nucleotide sequence of UNQ291 (DNA40594-1233) is shown in Figure 19 (SEQ ID NO:44). Clone UNQ291 (DNA40594-1233) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 9-11 and ending at the stop codon at nucleotide positions 1086-1088 (Figure 19). The predicted polypeptide precursor is 359 amino acids long (Figure 20). The full-length PRO329 protein shown in Figure 20 has an estimated molecular weight of about 38,899 daltons and a pI of about 5.21. Clone UNQ291 (DNA40594-1233) has been deposited with ATCC on February 5, 1998 and is assigned ATCC deposit no. 209617.

Analysis of the amino acid sequence of the full-length PRO329 polypeptide suggests that it possesses significant sequence similarity to a high affinity immunoglobulin F_c receptor protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO329 amino acid sequence and the following Dayhoff sequences, FCG1_HUMAN, FCG0_HUMAN, P_R91439, P_R22549, P_R91438, P_W00859, P_R20811, P_R22550, HUMCD6406_1 and FCG1_MOUSE.

<u>EXAMPLE 9</u>: <u>Isolation of cDNA Clones Encoding Human PRO362</u>

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA42257. Based on the DNA42257 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO362.

PCR primers (forward and reverse) were synthesized:

<u>forward PCR primer 1 (42257.f1)</u> 5'-TATCCCTCCAATTGAGCACCCTGG-3' (SEQ ID NO:53)
<u>forward PCR primer 2 (42257.f2)</u> 5'-GTCGGAAGACATCCCAACAAG-3' (SEQ ID NO:54)
<u>reverse PCR primer 1 (42257.r1)</u> 5'-CTTCACAATGTCGCTGTGCTGCTC-3' (SEQ ID NO:55)
<u>reverse PCR primer 2 (42257.r2)</u> 5'-AGCCAAATCCAGCAGCTGGCTTAC-3' (SEQ ID NO:56)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA42257 sequence which had the following nucleotide sequence

<u>hybridization probe (42257.p1)</u>
5'-TGGATGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCCTGAT-3' (SEQ ID NO:57)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO362 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal brain tissue (LIB153).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO362 [herein designated as UNQ317 (DNA45416-1251)] (SEQ ID NO:51) and the derived protein sequence for PRO362.

The entire nucleotide sequence of UNQ317 (DNA45416-1251) is shown in Figure 21 (SEQ ID NO:51). Clone UNQ317 (DNA45416-1251) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 119-121 and ending at the stop codon at nucleotide positions 1082-1084 (Figure 21). The predicted polypeptide precursor is 321 amino acids long (Figure 22). The full-length PRO362 protein shown in Figure 2 has an estimated molecular weight of about 35,544 daltons and a pI of about 8.51. Analysis of the full-length PRO362 polypeptide as shown in Figure 22 evidences the presence of a glycosaminoglycan attachment site at about amino acid 149 to about amino acid 152 and a transmembrane domain from about amino acid 276 to about amino acid 306.. Clone UNQ317 (DNA45416-1251) has been deposited with ATCC on February 5, 1998 and is assigned ATCC deposit no. 209620.

Analysis of the amino acid sequence of the full-length PRO362 polypeptide suggests that it possesses significant sequence similarity to the A33 antigen protein and the HCAR protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO362 amino acid sequence and the following Dayhoff sequences, AB002341_1, HSU55258_1, HSC7NRCAM_1, RNU81037_1, A33_HUMAN, P_W14158, NMNCAMRI_1, HSTITINN2_1, S71824_1 and HSU63041_1.

EXAMPLE 10: Isolation of cDNA Clones Encoding Human PRO363

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA42828. Based on the DNA42828 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO363.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer (42828.f1) 5'-CCAGTGCACAGCAGGCAACGAAGC-3' (SEQ ID NO:60)

reverse PCR primer (42828.r1) 5'-ACTAGGCTGTATGCCTGGGTGGGC-3' (SEQ ID NO:61)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA42828 sequence which had the following nucleotide sequence

hybridization probe (42828.p1)

5'-GTATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGC-3' (SEQ ID NO:62)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO363 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO363 [herein designated as UNQ318 (DNA45419-1252)] (SEQ ID NO:58) and the derived protein sequence for PRO363.

The entire nucleotide sequence of UNQ318 (DNA45419-1252) is shown in Figure 23 (SEQ ID NO:58). Clone UNQ318 (DNA45419-1252) contains a single open reading frame with an apparent translational initiation

site at nucleotide positions 190-192 and ending at the stop codon at nucleotide positions 1309-1311 (Figure 23). The predicted polypeptide precursor is 373 amino acids long (Figure 24). The full-length PRO363 protein shown in Figure 24 has an estimated molecular weight of about 41,281 daltons and a pI of about 8.33. A transmembrane domain exists at amino acids 221 to 254 of the amino acid sequence shown in Figure 24 (SEQ ID NO:59). The PRO363 polypeptide also possesses at least two myelin P0 protein domains from about amino acids 15 to 56 and from about amino acids 87 to 116. Clone UNQ318 (DNA45419-1252) has been deposited with ATCC on February 5, 1998 and is assigned ATCC deposit no. 209616.

Analysis of the amino acid sequence of the full-length PRO363 polypeptide suggests that it possesses significant sequence similarity to the cell surface protein HCAR, thereby indicating that PRO363 may be a novel HCAR homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO363 amino acid sequence and the following Dayhoff sequences, HS46KDA_1, HSU90716_1, MMCARH_1, MMCARHOM_1, MMU90715_1, A33_HUMAN, P_W14146, P_W14158, A42632 and B42632.

<u>EXAMPLE 11</u>: <u>Isolation of cDNA Clones Encoding Human PRO868</u>

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA38133. Based on the DNA38133 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO868.

A pair of PCR primers (forward and reverse) were synthesized:

<u>forward PCR primer (38133.f1)</u> 5'-GTAGCAGTGCACATGGGGTGTTGG-3' (SEQ ID NO:65)

<u>reverse PCR primer (38133.r1)</u> 5'-ACCGCACATCCTCAGTCTCTGTCC-3' (SEQ ID NO:66)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA38133 sequence which had the following nucleotide sequence

<u>hybridization probe (38133.p1)</u>

5'-ACGATGATCGCGGGCTCCCTTCTCCTGCTTGGATTCCTTAGCACCACCAC-3' (SEQ ID NO:67)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO868 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO868 [herein designated as UNQ437 (DNA52594-1270)] (SEQ ID NO:63) and the derived protein sequence for PRO868.

The entire nucleotide sequence of UNQ437 (DNA52594-1270) is shown in Figure 25 (SEQ ID NO:63). Clone UNQ437 (DNA52594-1270) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 325-327 and ending at the stop codon at nucleotide positions 2290-2292 (Figure 25).

The predicted polypeptide precursor is 655 amino acids long (Figure 26). The full-length PRO868 protein shown in Figure 26 has an estimated molecular weight of about 71,845 daltons and a pI of about 8.22. Analysis of the full-length PRO868 polypeptide sequence demonstrates the presence of conserved cysteine-containing domains from about amino acid 66 to about amino acid 78 and from about amino acid 123 to about amino acid 134 of the sequence shown in Figure 26 (SEQ ID NO:3), a TNFR death domain from about amino acid 85 to about amino acid 110, a FASA_mouse death domain block from about amino acid 159 to about amino acid 175 and a transmembrane domain from about amino acid 347 to about amino acid 375. Clone UNQ437 (DNA52594-1270) has been deposited with ATCC on March 17, 1998 and is assigned ATCC deposit no. 209679

Analysis of the amino acid sequence of the full-length PRO868 polypeptide suggests that it possesses significant sequence similarity to the tumor necrosis factor receptor protein, thereby indicating that PRO868 may be a novel member of the tumor necrosis factor receptor family. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO868 amino acid sequence and the following Dayhoff sequences, RNU94330_1, P_R99933, P_R99945, P_R99950, HSU94332_1, CD40_HUMAN, S63368_1, TNR2_HUMAN, MVU87844_1 AND CVU87837_1.

EXAMPLE 12: Isolation of cDNA Clones Encoding Human PRO382

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA30892. Based on the DNA30892 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO382.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-TGACATCGCCCTTATGAAGCTGGC-3' (SEQ ID NO:70)

reverse PCR primer 5'-TACACGTCCCTGTGGTTGCAGATC-3' (SEQ ID NO:71)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30892 sequence which had the following nucleotide sequence

hybridization probe

5'-CGTTCAATGCAGAAATGATCCAGCCTGTGTGCCTGCCCAACTCTGAAGAG-3' (SEQ ID NO:72)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO382 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO382 [herein designated as UNQ323 (DNA45234-1277)] (SEQ ID NO:68) and the derived protein sequence for PRO382.

The entire nucleotide sequence of UNQ323 (DNA45234-1277) is shown in Figure 27 (SEQ ID NO:68). Clone UNQ323 (DNA45234-1277) contains a single open reading frame with an apparent translational initiation

site at nucleotide positions 126-128 and ending at the stop codon at nucleotide positions 1485-1487 (Figure 27). The predicted polypeptide precursor is 453 amino acids long (Figure 28). The full-length PRO382 protein shown in Figure 28 has an estimated molecular weight of about 49,334 daltons and a pI of about 6.32. Analysis of the native PRO382 amino acid sequence shown in Figure 28 (SEQ ID NO:69) indicates the presence of a putative transmembrane domain from about amino acid 240 to about amino acid 284, a putative signal peptide at about amino acid 1 to about amino acid 20, a putative apple domain at about amino acid 386 to about amino acid 419, a putative Kringle domain at about amino acid 394 to about amino acid 406 and a histidine-containing protease active site at about amino acid 253 to about amino acid 258. Clone UNQ323 (DNA45234-1277) has been deposited with ATCC on March 5, 1998 and is assigned ATCC deposit no. 209654.

Analysis of the amino acid sequence of the full-length PRO382 polypeptide suggests that it possess significant homology to serine protease proteins, thereby indicating that PRO382 may be a novel serine protease. Specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO382 amino acid sequence and the following Dayhoff sequences, HSU75329_1, ENTK_MOUSE, HEPS_HUMAN, AF030065_1, HEPS_RAT, PLMN_PIG, P_R89430, P_R89435, PLMN_HORSE, PLMN_BOVIN and P_R83959.

EXAMPLE 13: Isolation of cDNA Clones Encoding Human PRO545

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA44706. An EST proprietary to Genentech was employed in the consensus assembly and is herein designated DNA13217 (Figure 31; SEQ ID NO:75). Based on the DNA44706 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO545.

Forward and reverse PCR primers were synthesized:

forward PCR primer 1 5'-GTCTCAGCACGTGTTCTGGTCTCAGGG-3' (SEQ ID NO:76)
forward PCR primer 2 5'-CATGAGCATGTGCACGGC-3' (SEQ ID NO:77)
forward PCR primer 3 5'-TACCTGCACGATGGGCAC-3' (SEQ ID NO:78)
forward PCR primer 4 5'-CACTGGGCACCTCCCTTC-3' (SEQ ID NO:79)
reverse PCR primer 1 5'-CTCCAGGCTGGTCTCCAAGTCCTTCC-3' (SEQ ID NO:80)
reverse PCR primer 2 5'-TCCCTGTTGGACTCTGCAGCTTCC-3' (SEQ ID NO:81)
reverse PCR primer 3 5'-CTTCGCTGGGAAGAGTTTG-3' (SEQ ID NO:82)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA44706 sequence which had the following nucleotide sequence

hybridization probe

5'-GTGCAACCAACAGATACAAACTCTTCCCAGCGAAGAAGCTGAAAAGCGTC-3' (SEQ ID NO:83)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was

screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO545 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human placenta tissue (LIB90).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO545 [herein designated as UNQ346 (DNA49624-1279)] (SEQ ID NO:73) and the derived protein sequence for PRO545.

The entire nucleotide sequence of UNQ346 (DNA49624-1279) is shown in Figure 29 (SEQ ID NO:73). Clone UNQ346 (DNA49624-1279) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 311-313 and ending at the stop codon at nucleotide positions 2516-2518 (Figure 29). The predicted polypeptide precursor is 735 amino acids long (Figure 30). The full-length PRO545 protein shown in Figure 30 has an estimated molecular weight of about 80,177 daltons and a pI of about 7.08. Important regions of the PRO545 amino acid sequence include the signal peptide, corresponding to amino acids 1-28, five potential N-glycosylation sites, from about amino acid 111-114, amino acids 146-149, amino acids 348-351, amino acids 449-452, and amino acids 648-651, and a neutral zinc metallopeptidase, zinc-binding region signature sequence, from about amino acids 344-353. Clone UNQ346 (DNA49624-1279) has been deposited with ATCC and is assigned ATCC deposit no. 209655.

EXAMPLE 14: Isolation of cDNA Clones Encoding Human PRO617

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA42798. Based on the DNA42798 sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO617.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-ACGGGCACACTGGATCCCAAATG-3' (SEQ ID NO:86)

reverse PCR primer 5'-GGTAGAGATGTAGAAGGGCAAGCAAGACC-3' (SEQ ID NO:87)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA42798 sequence which had the following nucleotide sequence

hybridization probe

5'-GCTCCCTACCCGTGCAGGTTTCTTCATTTGTTCCTTTAACCAGTATGCCG-3' (SEQ ID NO:88)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO617 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO617 [herein designated as UNQ353 (DNA48309-1280)] (SEQ ID NO:1) and the derived protein sequence for PRO617.

The entire nucleotide sequence of UNQ353 (DNA48309-1280) is shown in Figure 32 (SEQ ID NO:84).

Clone UNQ353 (DNA48309-1280) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 723-725 and ending at the stop codon at nucleotide positions 924-926 (Figure 32). The predicted polypeptide precursor is 67 amino acids long (Figure 33). The full-length PRO617 protein shown in Figure 33 has an estimated molecular weight of about 6,981 daltons and a pI of about 7.47. Analysis of the PRO617 amino acid sequence also evidences the existence of a putative signal peptide from about amino acid 15 to about amino acid 27 and a putative protein kinase C phosphorylation site from about amino acid 41 to about amino acid 43. Clone UNQ353 (DNA48309-1280) has been deposited on March 5, 1998 with ATCC and is assigned ATCC deposit no. 209656.

Analysis of the amino acid sequence of the full-length PRO617 polypeptide suggests that it possesses significant homology to the CD24 protein, thereby indicating that PRO617 may be a novel CD24 homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO617 amino acid sequence and the following Dayhoff sequences, CD24_HUMAN, CD24_MOUSE, S15785, CD24_RAT, VGE BPG4, MSE5_HUMAN, HSMHC3W36A_2, MLU15184_8, P R85075, SEPL_HUMAN and MTCY63_13.

EXAMPLE 15: Isolation of cDNA Clones Encoding Human PRO700

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA30837. Based on the DNA30837 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO700.

Forward and reverse PCR primers were synthesized:

forward PCR primer 1 5'-ATGTTCTTCGCGCCCTGGTG-3' (SEQ ID NO:91)

forward PCR primer 2 5'-CCAAGCCAACACACTCTACAG-3' (SEQ ID NO:92)

reverse PCR primer 1 5'-AAGTGGTCGCCTTGTGCAACGTGC-3' (SEQ ID NO:93)

reverse PCR primer 2 5'-GGTCAAAGGGGATATATCGCCAC-3' (SEQ ID NO:94)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30837 sequence which had the following nucleotide sequence

hybridization probe

5'-GCATGGAAGATGCCAAAGTCTATGTGGCTAAAGTGGACTGCACGGCCCA-3' (SEQ ID NO:95)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO700 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for

PRO700 [herein designated as UNQ364 (DNA46776-1284)] (SEQ ID NO:89) and the derived protein sequence for PRO700.

The entire nucleotide sequence of UNQ364 (DNA46776-1284) is shown in Figure 34 (SEQ ID NO:89). Clone UNQ364 (DNA46776-1284) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 33-35 and ending at the stop codon at nucleotide positions 1329-1331 (Figure 34). The predicted polypeptide precursor is 432 amino acids long (Figure 35). The full-length PRO700 protein shown in Figure 35 has an estimated molecular weight of about 47,629 daltons and a pI of about 5.90. Important regions of the amino acid sequence of PRO700 include the signal peptide, corresponding to amino acids from about 1 to 33; regions homologous to disulfide isomerase, corresponding to amino acids from about 82-99, 210-255, and 345-360, a tyrosine kinase phosphorylation site, corresponding to amino acids from about 143-151, and an endoplasmic reticulum targeting sequence, corresponding to amino acids from about 429-432. Clone UNQ364 (DNA46776-1284) has been deposited with ATCC and is assigned ATCC Deposit No. 209721.

EXAMPLE 16: Isolation of cDNA Clones Encoding Human PRO702

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA36623. Based on the DNA36623 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO702.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer (36623.f1) 5'-CGCTGACTATGTTGCCAAGAGTGG-3' (SEQ ID NO:98)

reverse PCR primer (36623.r1) 5'-GATGATGGAGGCTCCATACCTCAG-3' (SEQ ID NO:99)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA36623 sequence which had the following nucleotide sequence

hybridization probe (36623.p1)

5'-GTGTTCATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACATGTTCAC-3' (SEQ ID NO:100)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO702 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal liver tissue (LIB229).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO702 [herein designated as UNQ366 (DNA50980-1286)] (SEQ ID NO:96) and the derived protein sequence for PRO702.

The entire nucleotide sequence of UNQ366 (DNA50980-1286) is shown in Figure 36 (SEQ ID NO:96). Clone UNQ366 (DNA50980-1286) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 22-24 and ending at the stop codon at nucleotide positions 853-855 (Figure 36). The predicted polypeptide precursor is 277 amino acids long (Figure 37). The full-length PRO702 protein shown

in Figure 37 has an estimated molecular weight of about 30,645 daltons and a pI of about 7.47. Analysis of the full-length native PRO702 amino acid sequence evidences the presence of a putative signal peptide from about amino acid 1 to about amino acid 25, potential N-glycosylation sites from about amino acid 230 to about amino acid 233 and from about amino acid 258 to about amino acid 261 and a C-type lectin domain signature sequence from about amino acid 248 to about amino acid 270. Clone UNQ366 (DNA50980-1286) has been deposited with ATCC on March 31, 1998 and is assigned ATCC deposit no. 209717.

Analysis of the amino acid sequence of the full-length PRO702 polypeptide suggests that it possesses significant sequence similarity to the conglutinin protein, thereby indicating that PRO702 may be a novel conglutinin homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO702 amino acid sequence and the following Dayhoff sequences, S32436, P_R75642, P _W18780, P_W18781, A53330, AC002528_1, HSPPA2IC0_1, CA21_HUMAN, CA14_HUMAN and A61262.

EXAMPLE 17: Isolation of cDNA Clones Encoding Human PRO703

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA43047. Based on the DNA43047 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO703.

Forward and reverse PCR primers were synthesized:

forward PCR primer 5'-GAGAGCCATGGGGCTCCACCTG-3' (SEQ ID NO:103)
reverse PCR primer 1 5'-GGAGAATGTGGCCACAAC-3' (SEQ ID NO:104)
reverse PCR primer 2 5'-GCCCTGGCACAGTGACTCCATAGACG-3' (SEQ ID NO:105)
reverse PCR primer 3 5'-ATCCACTTCAGCGGACAC-3' (SEQ ID NO:106)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA40654 sequence which had the following nucleotide sequence

hybridization probe
5'-CCAGTGCCAGGATACCTCTCTTCCCCCCAGAGCATAACAGACACG-3'
(SEQ ID NO:107)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO703 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO703 [herein designated as UNQ367 (DNA50913-1287)] (SEQ ID NO:101) and the derived protein sequence for PRO703.

The entire nucleotide sequence of UNQ367 (DNA50913-1287) is shown in Figure 38 (SEQ ID

NO:101). Clone UNQ367 (DNA50913-1287) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 115-117 and ending at the stop codon at nucleotide positions 2305-2307 (Figure 38). The predicted polypeptide precursor is 730 amino acids long (Figure 39). The full-length PRO703 protein shown in Figure 39 has an estimated molecular weight of about 78,644 daltons, and a pI of about: 7.65. Important regions of the PRO703 amino acid sequence include the signal peptide, a cAMP- and cGMP-dependent protein kinase phosphorylation site, a CUB domain protein motif, N-glycosylation sites and a putative AMP-binding domain signature. Clone UNQ367 (DNA50913-1287) has been deposited with ATCC and is assigned ATCC deposit no. 209716.

EXAMPLE 18: Isolation of cDNA Clones Encoding Human PRO705

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA43437. Based on the DNA43437 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO705.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-AAGCGTGACAGCGGGCACGTC-3' (SEQ ID NO:110)

reverse PCR primer 5'-TGCACAGTCTCTGCAGTGCCCAGG-3' (SEQ ID NO:111)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA43437 sequence which had the following nucleotide sequence

hybridization probe (43437.p1)

5'-GAATGCTGGAACGGGCACAGCAAAGCCAGATACTTGCCTG-3' (SEQ ID NO:112)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO705 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO705 [herein designated as UNQ369 (DNA50914-1289)] (SEQ ID NO:108) and the derived protein sequence for PRO705.

The entire nucleotide sequence of UNQ369 (DNA50914-1289) is shown in Figure 40 (SEQ ID NO:108). Clone UNQ369 (DNA50914-1289) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 566-568 and ending at the stop codon at nucleotide positions 2231-2233 (Figure 40). The predicted polypeptide precursor is 555 amino acids long (Figure 41). The full-length PRO705 protein shown in Figure 41 has an estimated molecular weight of about 62,736 daltons and a pI of about 5.36. Analysis of the full-length PRO705 sequence as shown in Figure 41 evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 23, a eukaryotic DNA topoisomerase I active site from about amino acid 418 to about amino acid 436, and various regions that show homology to various glypican

proteins from about amino acid 237 to about amino acid 279, about amino acid 421 to about amino acid 458, about amino acid 53 to about amino acid 74, about amino acid 466 to about amino acid 504, about amino acid 308 to about amino acid 355, about amino acid 104 to about amino acid 156 and about amino acid 379 to about amino acid 410. Clone UNQ369 (DNA50914-1289) has been deposited with ATCC on March 31, 1998 and is assigned ATCC deposit no.209722.

Analysis of the amino acid sequence of the full-length PRO705 polypeptide suggests that it possesses significant sequence similarity to the K-glypican protein, thereby indicating that PRO705 may be a novel glypican protein family member. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO705 amino acid sequence and the following Dayhoff sequences, GPCK_MOUSE, GLYP_CHICK, GLYP_RAT, GLYP_HUMAN, GPC2_RAT, GPC5_HUMAN, GPC3_HUMAN, GPC3_RAT, P_R30168 and CEC03H12_2.

EXAMPLE 19: Isolation of cDNA Clones Encoding Human PRO708

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA34024. Based on the DNA34024 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO708.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CCCAACCCAACTGTTTACCTCTGG-3' (SEQ ID NO:115)

reverse PCR primer 5'-CTCTCTGAGTGTACATCTGTGTGG-3' (SEQ ID NO:116)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA34024 sequence which had the following nucleotide sequence

hybridization probe

5'-GCCACCCTACCTCAGAAACTGAAGGAGGTTGGNTATTCAACGCATATGGTCGG-3' (SEQ ID NO:117)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO708 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human bone marrow tissue (LIB255).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO708 [herein designated as UNQ372 (DNA48296-1292)] (SEQ ID NO:113) and the derived protein sequence for PRO708.

The entire nucleotide sequence of UNQ372 (DNA48296-1292) is shown in Figures 42A-B (SEQ ID NO:113). Clone UNQ372 (DNA48296-1292) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 891-893 and ending at the stop codon at nucleotide positions 2436-2438 (Figures 42A-B). The predicted polypeptide precursor is 515 amino acids long (Figure 43). The full-length

PRO708 protein shown in Figure 43 has an estimated molecular weight of about 56,885 daltons and a pI of about 6.49. Analysis of the PRO708 amino acid sequence shown in Figure 43 (SEQ ID NO:114) evidences the existence of a putative signal peptide at about amino acid 1 to about amino acid 37, putative sulfatase signature sequences at about amino acid 120 to about amino acid 132 and about amino acid 168 to about amino acid 177, a putative tyrosine kinase phosphorylation site from about amino acid 163 to about amino acid 169 and potential N-glycosylation sites from about amino acid 157 to about amino acid 160, about amino acid 306 to about amino acid 309 and about amino acid 318 to about amino acid 321. Clone UNQ372 (DNA48296-1292) has been deposited with ATCC on March 11, 1998 and is assigned ATCC deposit no. 209668.

Analysis of the amino acid sequence of the full-length PRO708 polypeptide suggests that it possesses significant homology to the aryl sulfatase proteins, thereby indicating that PRO708 may be a novel aryl sulfatase homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO708 amino acid sequence and the following Dayhoff sequences, ARSB_HUMAN, CELC54D2_2, G02857, STS_HUMAN, I37186, I37187, GEN12648, CELD1014_7, GA6S_HUMAN and SPHM_HUMAN.

EXAMPLE 20: Isolation of cDNA Clones Encoding Human PRO320

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA28739. Based on the DNA28739 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO320.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CCTCAGTGGCCACATGCTCATG-3' (SEQ ID NO:120)

reverse PCR primer 5'-GGCTGCACGTATGGCTATCCATAG-3' (SEQ ID NO:121)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA28739 sequence which had the following nucleotide sequence

hybridization probe

5'-GATAAACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCC-3' (SEQ ID NO:122)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO320 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal lung tissue (LIB25).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO320 [herein designated as UNQ281 (DNA32284-1307)] (SEQ ID NO:118) and the derived protein sequence for PRO320.

The entire nucleotide sequence of UNQ281 (DNA32284-1307) is shown in Figure 44 (SEQ ID NO:118). Clone UNQ281 (DNA32284-1307) contains a single open reading frame with an apparent translational

initiation site at nucleotide positions 135-137 and ending at the stop codon at nucleotide positions 1149-1151 (Figure 44). The predicted polypeptide precursor is 338 amino acids long (Figure 45). The full-length PRO320 protein shown in Figure 45 has an estimated molecular weight of about 37,143 daltons and a pI of about 8.92. Important regions of the PRO320 amino acid sequence include the signal peptide, corresponding to amino acids 1-21, an EGF-like domain cysteine pattern signature, corresponding to amino acids 80-91, and three calcium-binding EGF-like domains, corresponding to amino acids 103-124, 230-151 and 185-206, respectively. Clone UNQ281 (DNA32284-1307) has been deposited with ATCC and is assigned ATCC deposit no. 209670.

EXAMPLE 21: Isolation of cDNA Clones Encoding Human PRO324

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA34347. Based on the DNA34347 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO324.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 5'-GCAATGAACTGGGAGCTGC-3' (SEQ ID NO:125)
forward PCR primer 2 5'-CTGTGAATAGCATCCTGGG-3' (SEQ ID NO:126)
forward PCR primer 3 5'-CTTTTCAAGCCACTGGAGGG-3' (SEQ ID NO:127)
reverse PCR primer 1 5'-CTGTAGACATCCAAGCTGGTATCC-3' (SEQ ID NO:128)
reverse PCR primer 2 5'-AAGAGTCTGCATCCACACCACTC-3' (SEQ ID NO:129)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA34347 sequence which had the following nucleotide sequence

hybridization probe
5'-ACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCCAGAATG-3' (SEQ ID NO:130)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO324 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal liver tissue (LIB6).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO324 [herein designated as UNQ285 (DNA36343-1310)] (SEQ ID NO: 123) and the derived protein sequence for PRO324.

The entire nucleotide sequence of UNQ285 (DNA36343-1310) is shown in Figure 46 (SEQ ID NO:123). Clone UNQ285 (DNA36343-1310) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 144-146 and ending at the stop codon at nucleotide positions 1011-1013 (Figure 46). The predicted polypeptide precursor is 289 amino acids long (Figure 47). The full-length PRO324 protein shown in Figure 47 has an estimated molecular weight of about 32,268 daltons and a pI of about 9.21. Analysis of the PRO324 polypeptide sequence shown in Figure 47 (SEQ ID NO:124) evidence the presence of

the following: a signal peptide from about amino acid 1 to about amino acid 31, a transmembrane domain from about amino acid 136 to about amino acid 157, tyrosine kinase phosphorylation sites from about amino acid 106 or about amino acid 107 to about amino acid 113 and regions that are homologous to short-chain alcohol dehydrogenase regions from about amino acid 80 to about amino acid 90, from about amino acid 131 to about amino acid 168, from about amino acid 1 to about amino acid 13 and from about amino acid 176 to about amino acid 185. Clone UNQ285 (DNA36343-1310) has been deposited with ATCC on March 30, 1998 and is assigned ATCC deposit no. 209718.

Analysis of the amino acid sequence of the full-length PRO324 polypeptide suggests that it possesses significant sequence similarity to oxidoreductases, thereby indicating that PRO324 may be a novel oxidoreductase homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO324 amino acid sequence and the following Dayhoff sequences, B61209, A69965, YQJQ_BACSU, D69930, S76124, FABG_ECOLI, C70023, S77280, FABG_VIBHA and MTV013_6.

EXAMPLE 22: Isolation of cDNA Clones Encoding Human PRO351

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA35950. Based on the DNA35950 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO351.

Forward and reverse PCR primers were synthesized:

forward PCR primer 5'-CCTGTGCTGTGCCTCGAGCCTGAC-3' (SEQ ID NO:133)

reverse PCR primer 5'-GTGGGCAGCAGTTAGCACCGCCTC-3' (SEQ ID NO:134)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35950 sequence which had the following nucleotide sequence

hybridization probe

5'-GGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGC-3'

(SEQ ID NO:135)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO351 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal liver tissue (LIB230).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO351 [herein designated as UNQ308 (DNA40571-1315)] (SEQ ID NO:131) and the derived protein sequence for PRO351.

The entire nucleotide sequence of UNQ308 (DNA40571-1315) is shown in Figure 48 (SEQ ID NO:131). Clone UNQ308 (DNA40571-1315) contains two open reading frames with an apparent translational initiation site at nucleotide positions 189-191 and a second open reading frame beginning at nucleotide 470, with

the two open reading frames ending at the stop codons at nucleotide positions 363-365 and 2009-2011, respectively (Figure 48). The predicted polypeptide precursor is 571 amino acids long (Figure 49). Important regions of the amino acid sequence of PRO351 include the signal peptide, regions having sequence similarity to serine proteases of the trypsin family, two N-glycosylation sites, and three Kringle domains. Clone UNQ308 (DNA40571-1315) has been deposited with ATCC and is assigned ATCC deposit no. 209784.

EXAMPLE 23: Isolation of cDNA Clones Encoding Human PRO352

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA36950. Based on the DNA36950 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO352.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 5'-CTGGCACAGCTCAACCTCATCTGG-3' (SEQ ID NO:138)
forward PCR primer 2 5'-GCTGTCTGTCTGTCTCATTG-3' (SEQ ID NO:139)
forward PCR primer 3 5'-GGACACAGTATACTGACCAC-3' (SEQ ID NO:140)
reverse PCR primer 1 5'-TGCGAACCAGGCAGCTGTAAGTGC-3' (SEQ ID NO:141)
reverse PCR primer 2 5'-TGGAAGAAGAGGGTGGTGATGTGG-3' (SEQ ID NO:142)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA36950 sequence which had the following nucleotide sequence

hybridization probe
5'-CAGCTGACAGACACCAAACAGCTGGTGCACAGTTTCACCGAAGGC-3' (SEQ ID NO:143)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO352 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO352 [herein designated as UNQ309 (DNA41386-1316)] (SEQ ID NO:136) and the derived protein sequence for PRO352.

The entire nucleotide sequence of UNQ309 (DNA41386-1316) is shown in Figure 50 (SEQ ID NO:136). Clone UNQ309 (DNA41386-1316) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 152-154 and ending at the stop codon at nucleotide positions 1100-1102 (Figure 50). The predicted polypeptide precursor is 316 amino acids long (Figure 51). The full-length PRO352 protein shown in Figure 2 has an estimated pI of about 4.62. Analysis of the full-length PRO352 sequence evidences the presence of a signal peptide from about amino acid 1 to about amino acid 28, a transmembrane domain from about amino acid 251 to about amino acid 270, potential N-glycosylation sites from about amino acid 91 to about amino acid 94, about amino acid 104 to about amino acid 107, about amino acid 189 to about

amino acid 192 and about amino acid 215 to about amino acid 218 and a region having homology to immunoglobulins and MHC from about amino acid 217 to about amino acid 234. Clone UNQ309 (DNA41386-1316) has been deposited with ATCC on March 26, 1998 and is assigned ATCC deposit no. 209703.

Analysis of the amino acid sequence of the full-length PRO352 polypeptide suggests that it possesses significant sequence similarity to the butyrophilin protein, thereby indicating that PRO352 is a novel butyrophilin homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO352 amino acid sequence and the following Dayhoff sequences, BUTY_HUMAN, HSB73_1, GGCD80_1, I46690, A33_HUMAN, P_R67988, CD86_MOUSE, P_R71360, B39371 and D50558_1.

EXAMPLE 24: Isolation of cDNA Clones Encoding Human PRO381

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA39651. Based on the DNA39651 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO381.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CTTTCCTTGCTTCAGCAACATGAGGC-3' (SEQ ID NO:146)

reverse PCR primer 5'-GCCCAGAGCAGGAGGAATGATGAGC-3' (SEQ ID NO:147)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA39651 sequence which had the following nucleotide sequence

hybridization probe

5'-GTGGAACGCGGTCTTGACTCTGTTCGTCACTTCTTTGATTGGGGCTTTG-3' (SEQ ID NO:148)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO381 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO381 [herein designated as UNQ322 (DNA44194-1317)] (SEQ ID NO:144) and the derived protein sequence for PRO381.

The entire nucleotide sequence of UNQ322 (DNA44194-1317) is shown in Figure 52 (SEQ ID NO:144). Clone UNQ322 (DNA44194-1317) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 174-176 and ending at the stop codon at nucleotide positions 807-809 (Figure 52). The predicted polypeptide precursor is 211 amino acids long (Figure 53). The full-length PRO381 protein shown in Figure 53 has an estimated molecular weight of about 24,172 daltons and a pI of about 5.99. Analysis of the full-length PRO381 polypeptide shown in Figure 53 (SEQ ID NO:145) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 20, a potential N-glycosylation

site from about amino acid 176 to about amino acid 179, potential casein kinase II phosphorylation sites from about amino acid 143 to about amino acid 146, from about amino acid 156 to about amino acid 159, from about amino acid 178 to about amino acid 181, and from about amino acid 200 to about amino acid 203, an endoplasmic reticulum targeting sequence from about amino acid 208 to about amino acid 211, FKBP-type peptidyl-prolyl cis-trans isomerase sites from about amino acid 78 to about amino acid 114 and from about amino acid 118 to about amino acid 131, EF-hand calcium binding domains from about amino acid 191 to about amino acid 203, from about amino acid 184 to about amino acid 203 and from about amino acid 140 to about amino acid 159, and an S-100/ICaBP type calcium binding domain from about amino acid 183 to about amino acid 203. Clone UNQ322 (DNA44194-1317) has been deposited with ATCC on April 28, 1998 and is assigned ATCC deposit no. 209808.

Analysis of the amino acid sequence of the full-length PRO381 polypeptide suggests that it possesses significant sequence similarity to FKBP immunophilin proteins, thereby indicating that PRO381 may be a novel FKBP immunophilin homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO381 amino acid sequence and the following Dayhoff sequences, AF040252_1, I49669, P_R93551, S71238, CELC05C8_1, CEU27353_1, MIP_TRYCR, CEZC455_3, FKB4_HUMAN and I40718.

EXAMPLE 25: Isolation of cDNA Clones Encoding Human PRO386

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA40674. Two proprietary Genentech EST sequences were employed in the consensus sequence assembly, wherein those EST sequences are herein designated DNA23350 (Figure 56; SEQ ID NO:151) and DNA23536 (Figure 57; SEQ ID NO:152). Based on the DNA40674 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO386.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-ACGGAGCATGGAGGTCCACAGTAC-3' (SEQ ID NO:153)

reverse PCR primer 5'-GCACGTTTCTCAGCATCACCGAC-3' (SEQ ID NO:154)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA40674 sequence which had the following nucleotide sequence

hybridization probe

5'-CGCCTGCCCTGCACCTTCAACTCCTGCTACACAGTGAACCACAAACAGTT-3' (SEQ ID NO:155)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO386 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal brain tissue (LIB153).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for

PRO386 [herein designated as UNQ326 (DNA45415-1318)] (SEQ ID NO:149) and the derived protein sequence for PRO386.

The entire nucleotide sequence of UNQ326 (DNA45415-1318) is shown in Figure 54 (SEQ ID NO:149). Clone UNQ326 (DNA45415-1318) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 146-148 and ending at the stop codon at nucleotide positions 791-793 (Figure 54). The predicted polypeptide precursor is 215 amino acids long (Figure 55). The full-length PRO386 protein shown in Figure 55 has an estimated molecular weight of about 24,326 daltons and a pI of about 6.32. Analysis of the full-length PRO386 sequence shown in Figure 55 (SEQ ID NO:150) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 20, a transmembrane domain from about amino acid 161 to about amino acid 179, an immunoglobulin-like fold from about amino acid 83 to about amino acid 127 and potential N-glycosylation sites from about amino acid 42 to about amino acid 45, from about amino acid 66 to about amino acid 69 and from about amino acid 74 to about amino acid 77. Clone UNQ326 (DNA45415-1318) has been deposited with ATCC on April 28, 1998 and is assigned ATCC deposit no. 209810.

Analysis of the amino acid sequence of the full-length PRO386 polypeptide suggests that it possesses significant sequence similarity to the sodium channel beta-2 subunit, thereby indicating that PRO386 is a novel homolog thereof. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO386 amino acid sequence and the following Dayhoff sequences, A57843, MYP0_HUMAN, GEN14531, JC4024, HS46KDA_1, HSU90716_1, D86996_2, MUSIGLVD_1, DMU42768_1 and S19247.

EXAMPLE 26: Isolation of cDNA Clones Encoding Human PRO540

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA39631. Based on the DNA39631 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO540.

Forward and reverse PCR primers were synthesized:

forward PCR primer 5'-CTGGGGCTACACACGGGGTGAGG-3' (SEQ ID NO:158)

reverse PCR primer 5'-GGTGCCGCTGCAGAAAGTAGAGCG-3' (SEQ ID NO:159)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA40654 sequence which had the following nucleotide sequence

hybridization probe

5'-GCCCCAAATGAAAACGGGCCCTACTTCCTGGCCCTCCGCGAGATG-3'

(SEQ ID NO:160)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO540 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO540 [herein designated as UNQ341 (DNA44189-1322)] (SEQ ID NO:156) and the derived protein sequence for PRO540.

The entire nucleotide sequence of UNQ341 (DNA44189-1322) is shown in Figure 58 (SEQ ID NO:156). Clone UNQ341 (DNA44189-1322) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 21-23 and ending at the stop codon at nucleotide positions 1257-1259 (Figure 58). The predicted polypeptide precursor is 412 amino acids long (Figure 59). The full-length PRO540 protein shown in Figure 59 has an estimated molecular weight of about 46,658 daltons and a pI of about 6.65. Important regions of the amino acid sequence of PRO540 include the signal peptide, potential N-glycosylation sites, a potential lipid substrate binding site, a sequence typical of lipases and serine proteins, and a beta-transducin family Trp-Asp repeat. Clone UNQ341 (DNA44189-1322) has been deposited with ATCC and is assigned ATCC deposit no. 209699.

EXAMPLE 27: Isolation of cDNA Clones Encoding Human PRO615

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA42240. Based on the DNA42240 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO615.

Forward and reverse PCR primers were synthesized:

forward PCR primer 5'-TGGTCTTCGCCTTGATCGTGTTCT-3' (SEQ ID NO:163)
forward PCR primer 5'-GTGTACTGAGCGGCGGTTAG-3' (SEQ ID NO:164)
reverse PCR primer 5'-CTGAAGGTGATGGCTGCCCTCAC-3' (SEQ ID NO:165)
reverse PCR primer 5'-CCAGGAGGCTCATGGGAAAGTCC-3' (SEQ ID NO:166)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA42240 sequence which had the following nucleotide sequence:

hybridization probe
5'-CCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGATGCCT-3'
(SEQ ID NO:167)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO615 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human bone marrow tissue (LIB255).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO615 [herein designated as UNQ352 (DNA48304-1323)] (SEQ ID NO:161) and the derived protein sequence for PRO615.

The entire nucleotide sequence of UNQ352 (DNA48304-1323) is shown in Figure 60 (SEQ ID NO:161). Clone UNQ352 (DNA48304-1323) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 51-53 and ending at the stop codon at nucleotide positions 723-725 (Figure 60). The predicted polypeptide precursor is 224 amino acids long (Figure 61). The full-length PRO615 protein shown in Figure 61 has an estimated molecular weight of about 24,810 daltons and a pI of about 4.75. Important regions of the amino acid sequence of PRO615 include a type II transmembrane domain, corresponding to about amino acids 24-43, other transmembrane domains, corresponding to about amino acids 74-90, 108-126, and 145-161, respectively, and a potential N-glycosylation site, corresponding to about amino acids 97-100. Clone UNQ352 (DNA48304-1323) has been deposited with ATCC and is assigned ATCC deposit no. 209811.

EXAMPLE 28: Isolation of cDNA Clones Encoding Human PRO618

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA30900. Based on the DNA30900 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO618.

Forward and reverse PCR primers were synthesized:

forward PCR primer 5'-TAACAGCTGCCCACTGCTTCCAGG-3' (SEQ ID NO:171)

reverse PCR primer 5'-TAATCCAGCAGTGCAGGCCGGG-3' (SEQ ID NO:172)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30900 sequence which had the following nucleotide sequence.

hybridization probe

5'-ATGGCCTCCACGGTGCTGTGGACCGTGTTCCTGGGCAAGGTGTGGCAGAA-3'

(SEQ ID NO:173)

Screening of the above described library gave rise to the partial cDNA clone designated herein DNA35597 (SEQ ID NO:170). Extension of this sequence using repeated cycles of BLAST and phrap gave rise to a nucleotide sequence designated herein as DNA43335. Primers based upon the DNA43335 consensus sequence were then prepared as follows.

forward PCR primer 5'-TGCCTATGCACTGAGGAGGCAGAAG-3' (SEQ ID NO:174)

reverse PCR primer 5'-AGGCAGGGACACAGAGTCCATTCAC-3' (SEQ ID NO:175)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA43335 sequence which had the following nucleotide sequence

hybridization probe

5'-AGTATGATTTGCCGTGCACCCAGGGCCAGTGGACGATCCAGAACAGGAGG-3'

(SEQ ID NO:176)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was

screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate full length clones encoding the PRO618 gene using the second probe oligonucleotide and one of the second set of PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal liver tissue (LIB229).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO618 [herein designated as UNQ354 (DNA49152-1324)] (SEQ ID NO:168) and the derived protein sequence for PRO618.

The entire nucleotide sequence of UNQ354 (DNA49152-1324) is shown in Figure 62 (SEQ ID NO:168). Clone UNQ354 (DNA49152-1324) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 73-75 and ending at the stop codon at nucleotide positions 2479-2481 (Figure 62). The predicted polypeptide precursor is 802 amino acids long (Figure 63). The full-length PRO618 protein shown in Figure 63 has an estimated molecular weight of about 88,846 daltons and a pI of about 6.41. Important regions of the amino acid sequence of PRO618 include type II transmembrane domain, a sequence typical of a protease, trypsin family, histidine active site, multiple N-glycosylation sites, two sequences typical of a Kringle domain, two regions having sequence similarity to Kallikrein light chain, and a region having sequence similarity to low-density lipoprotein receptor. Clone UNQ354 (DNA49152-1324) has been deposited with ATCC and is assigned ATCC deposit no. 209813.

<u>EXAMPLE 29</u>: <u>Isolation of cDNA Clones Encoding Human PRO719</u>

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA44851. Based on the DNA44851 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO719.

A pair of PCR primers (forward and reverse) were synthesized:

<u>forward PCR primer</u> 5'-GTGAGCATGAGCGAGCCGTCCAC-3' (SEQ ID NO:179)

<u>reverse PCR primer</u> 5'-GCTATTACAACGGTTCTTGCGGCAGC-3' (SEQ ID NO:180)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA44851 sequence which had the following nucleotide sequence

<u>hybridization probe</u>

5'-TTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTGCCTTCCAG-3' (SEQ ID NO:181)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO719 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human placenta tissue (LIB90).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO719 [herein designated as UNQ387 (DNA49646-1327)] (SEQ ID NO:177) and the derived protein sequence

for PRO719.

The entire nucleotide sequence of UNQ387 (DNA49646-1327) is shown in Figure 65 (SEQ ID NO:177). Clone UNQ387 (DNA49646-1327) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 223-225 and ending at the stop codon at nucleotide positions 1285-1287 (Figure 65). The predicted polypeptide precursor is 354 amino acids long (Figure 66). The full-length PRO719 protein shown in Figure 66 has an estimated molecular weight of about 39,362 daltons and a pI of about 8.35. Analysis of the full length PRO719 sequence evidences the presence of a signal peptide from about amino acid 1 to about amino acid 16 as shown in Figure 66 (SEQ ID NO:178), a lipase-associated serine-containing active site at about amino acid 163 to about amino acid 172, and two potential N-glycosylation sites from about amino acid 80 to about amino acid 83 and about amino acid 136 to about amino acid 139. Clone UNQ387 (DNA49646-1327) has been deposited with ATCC on March 26, 1998 and is assigned ATCC deposit no. 209705.

Analysis of the amino acid sequence of the full-length PRO719 polypeptide suggests that it possesses significant sequence similarity to the lipoprotein lipase H protein, thereby indicating that PRO719 may be a novel lipoprotein lipase homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO719 amino acid sequence and the following Dayhoff sequences, LIPL_HUMAN, LIPH_HUMAN, D83548_1, A24059_1, P_R30740, D88666_1, A43357, A46696, B43357 and A49488.

EXAMPLE 30: Isolation of cDNA Clones Encoding Human PRO724

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA35603. Based on the DNA35603 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO724.

Pairs of PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 5'-GGCTGTCACTGTGGAGACAC-3' (SEQ ID NO:184)
forward PCR primer 2 5'-GCAAGGTCATTACAGCTG-3' (SEQ ID NO:185)
reverse PCR primer 1 5'-AGAACATAGGAGCAGTCCCACTC-3' (SEQ ID NO:186)
reverse PCR primer 2 5'-TGCCTGCTGCTGCACAATCTCAG-3' (SEQ ID NO:187)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35603 sequence which had the following nucleotide sequence:

hybridization probe

5'-GGCTATTGCTTGCCTTGGGACAGACCCTGTGGCTTAGGCTCTGGC-3' (SEQ ID NO:188)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO724 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal lung tissue (LIB26).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO724 [herein designated as UNQ389 (DNA49631-1328)] (SEQ ID NO:182) and the derived protein sequence for PRO724.

The entire nucleotide sequence of UNQ389 (DNA49631-1328) is shown in Figure 67 (SEQ ID NO:182). Clone UNQ389 (DNA49631-1328) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 546-548 and ending at the stop codon at nucleotide positions 2685-2687 (Figure 67). The predicted polypeptide precursor is 713 amino acids long (Figure 68). The full-length PRO724 protein shown in Figure 68 has an estimated molecular weight of about 76,193 daltons and a pI of about 5.42. Analysis of the full-length PRO724 amino acid sequence shown in Figure 68 (SEQ ID NO:183) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 16, a transmembrane domain from about amino acid 442 to about amino acid 462 and LDL receptor class A domain regions from about amino acid 152 to about amino acid 171, about amino acid 331 to about amino acid 350, about amino acid 374 to about amino acid 393 and about amino acid 411 to about amino acid 430. Clone UNQ389 (DNA49631-1328) has been deposited with ATCC on April 28, 1998 and is assigned ATCC deposit no. 209806

Analysis of the amino acid sequence of the full-length PRO724 polypeptide suggests that it possesses significant sequence similarity to the human LDL receptor protein, thereby indicating that PRO724 may be a novel LDL receptor homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO724 amino acid sequence and the following Dayhoff sequences, P_R48547, MMAM2R_1, LRP2_RAT, P_R60517, P_R47861, P_R05533, A44513_1, A30363, P_R74692 and LMLIPOPHO_1.

<u>EXAMPLE 31</u>: <u>Isolation of cDNA Clones Encoding Human PRO772</u>

One cDNA sequence was isolated in the amylase screen described in Example 2, wherein that cDNA sequence is herein designated DNA43509 (see Figure 71). Based on the DNA43509 sequence, oligonucleotide probes were generated and used to screen a human fetal lung library (LIB25) prepared as described in paragraph 1 of Example 2 above. The cloning vector was pRK5B (pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., <u>Science</u>, <u>253</u>:1278-1280 (1991)), and the cDNA size cut was less than 2800 bp.

A pair of PCR primers (forward and reverse) were synthesized based on the DNA43509 sequence:

<u>forward PCR primer</u> 5'-CGTTTTGCAGAACCTACTCAGGCAG-3' (SEQ ID NO:192)

<u>reverse PCR primer</u> 5'-CCTCCACCAACTGTCAATGTTGTGG-3' (SEQ ID NO:193)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA43509 sequence which had the following nucleotide sequence

<u>hybridization probe</u>

5'-AAAGTGCTGCTGCTGGGTCTGCAGACGCGATGGATAACGT-3' (SEQ ID NO:194)

Using the above described primers and library, a full length clone was identified that contained a single open reading frame with an apparent translational initiation site at nucleotide positions 131-133 and ending at the stop codon found at nucleotide positions 587-589 (Figure 69; SEQ ID NO:189). The predicted polypeptide

precursor is 152 amino acids long, has a calculated molecular weight of approximately 17,170 daltons and an estimated pI of approximately 9.62. Analysis of the full-length PRO772 sequence shown in Figure 70 (SEQ ID NO:190) evidences the presence of the following: a potential type II transmembrane domain from about amino acid 26 to about amino acid 42, other potential transmembrane domains from about amino acid 44 to about amino acid 65, from about amino acid 81 to about amino acid 101 and from about amino acid 109 to about amino acid 129, leucine zipper pattern sequences from about amino acid 78 to about amino acid 99 and from about amino acid 85 to about amino acid 106. Clone UNQ410 (DNA49645-1347) has been deposited with ATCC on April 28, 1998 and is assigned ATCC deposit no. 209809.

Analysis of the amino acid sequence of the full-length PRO772 polypeptide suggests that it possesses significant sequence similarity to the human A4 protein, thereby indicating that PRO772 may be a novel A4 protein homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO772 amino acid sequence and the following Dayhoff sequences, HSU93305_1, A4P_HUMAN, CELB0454_2, VPU_JSRV, CELC12D12_2, OCCM_AGRT1, LBPHIG1E_50, YIGK_ECOLI, S76245 and P_R50807.

EXAMPLE 32: Isolation of cDNA Clones Encoding Human PRO852

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA34364. Based on the DNA34364 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO852.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 5'-CGCAGAAGCTACAGATTCTCG-3' (SEQ ID NO:197)

forward PCR primer 2 5'-GGAAATTGGAGGCCAAAGC-3' (SEQ ID NO:198)

forward PCR primer 3 5'-GGATGTAGCCAGCAACTGTG-3' (SEQ ID NO:199)

forward PCR primer 4 5'-GCCTTGGCTCGTTCTCTTC-3' (SEQ ID NO:200)

forward PCR primer 5 5'-GGTCCTGTGCCTGGATGG-3' (SEQ ID NO:201)

reverse PCR primer 1 5'-GACAAGACTACCTCCGTTGGTC-3' (SEQ ID NO:202)

reverse PCR primer 2 5'-TGATGCACAGTTCAGCACCTGTTG-3' (SEQ ID NO:203)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA34364 sequence which had the following nucleotide sequence

hybridization probe

5'-CGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTG-3' (SEQ ID NO:204)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO852 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB228).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO852 [herein designated as UNQ418 (DNA45493-1349)] (SEQ ID NO:195) and the derived protein sequence for PRO852.

The entire nucleotide sequence of UNQ418 (DNA45493-1349) is shown in Figure 72 (SEQ ID NO:195). Clone UNQ418 (DNA45493-1349) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 94-96 and ending at the stop codon at nucleotide positions 16748-1650 (Figure 72). The predicted polypeptide precursor is 518 amino acids long (Figure 73). The full-length PRO852 protein shown in Figure 73 has an estimated molecular weight of about 56,180 daltons and a pI of about 5.08. Analysis of the full-length PRO852 sequence shown in Figure 73 (SEQ ID NO:196) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 20, a transmembrane domain from about amino acid 466 to about amino acid 494, potential N-glycosylation sites from about amino acid 170 to about amino acid 173 and about amino acid 366 to about amino acid 369, leucine zipper sequence pattern blocks from about amino acid 10 to about amino acid 31 and from about amino acid 197 to about amino acid 218 and blocks of amino acids having sequence homology to eukaryotic and viral aspartyl proteases from about amino acid 109 to about amino acid 118, from about amino acid 252 to about amino acid 261 and from about amino acid 298 to about amino acid 310. Clone UNQ418 (DNA45493-1349) has been deposited with ATCC on April 28, 1998 and is assigned ATCC deposit no. 209805.

Analysis of the amino acid sequence of the full-length PRO852 polypeptide suggests that it possesses significant sequence similarity to various protease proteins, thereby indicating that PRO852 may be a novel protease protein or homolog thereof. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO852 amino acid sequence and the following Dayhoff sequences, PEPC_HUMAN, S66516, S66517, PEPE_CHICK, CATD_HUMAN, P_R74207, CARP_YEAST, PEP2_RABIT, CATE_HUMAN and RENI_MOUSE.

<u>EXAMPLE 33</u>: <u>Isolation of cDNA Clones Encoding Human PRO853</u>

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA43050. Based on the DNA43050 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO853.

Forward and reverse PCR primers were synthesized:

<u>forward PCR primer</u> 5'-CTTCATGGCCTTGGACTTGGCCAG-3' (SEQ ID NO:207)

<u>reverse PCR primer</u> 5'-ACGCCAGTGGCCTCAAGCTGGTTG-3' (SEQ ID NO:208)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA43050 sequence which had the following nucleotide sequence

<u>hybridization probe</u>

5'-CTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGC-3' (SEQ ID NO:209)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO853 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB228).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO853 [herein designated as UNQ419 (DNA48227-1350)] (SEQ ID NO:205) and the derived protein sequence for PRO853.

The entire nucleotide sequence of UNQ419 (DNA48227-1350) is shown in Figure 74 (SEQ ID NO:205). Clone UNQ419 (DNA48227-1350) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 128-130 and ending at the stop codon at nucleotide positions 1259-1261 (Figure 74). The predicted polypeptide precursor is 377 amino acids long (Figure 75). The full-length PRO853 protein shown in Figure 75 has an estimated molecular weight of about 40,849 daltons and a pI of about 7.98. Important regions of the amino acid sequence of PRO853 include the signal peptide, corresponding to amino acids from about 1 to about 16 of SEQ ID NO:206, the glycosaminoglycan attachment site, corresponding to amino acids from about 46 to about 49 of SEQ ID NO:206, and two sequences typical of the short-chain alcohol dehydrogenase family, corresponding to amino acids from about 37 to about 49 and about 114 to about 124 of SEQ ID NO:206, respectively. Clone UNQ419 (DNA48227-1350) has been deposited with ATCC and is assigned ATCC deposit no. 209812.

EXAMPLE 34: Isolation of cDNA Clones Encoding Human PRO860

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA38137. Based on the DNA38137 consensu sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO860.

Forward and reverse PCR primers were synthesized:

forward PCR primer 5'-GAAGGGACCTACATGTGTGTGGCC-3' (SEQ ID NO:212)
reverse PCR primer 5'-ACTGACCTTCCAGCTGAGCCACAC-3' (SEQ ID NO:213)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA40654 sequence which had the following nucleotide sequence

hybridization probe
5'-AGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAA-3'
(SEQ ID NO:214)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO860 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal lung tissue (LIB26).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for

PRO860 [herein designated as UNQ421 (DNA41404-1352)] (SEQ ID NO:210) and the derived protein sequence for PRO860.

The entire nucleotide sequence of UNQ421 (DNA41404-1352) is shown in Figures 76A-B (SEQ ID NO:210). Clone UNQ421 (DNA41404-1352) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 58-60 and ending at the stop codon at nucleotide positions 3013-3015 (Figures 76A-B). The predicted polypeptide precursor is 985 amino acids long (Figure 77). The full-length PRO860 protein shown in Figure 77 has an estimated molecular weight of about 105,336 daltons and a pI of about 6.55. Important regions of the amino acid sequence of PRO860 include the transmembrane region corresponding to about amino acids 448-467, the extracellular domain, corresponding to amino acids about 1-447, several N-glycosylation sites, numerous N-myristoylation sites and a sequence typical of phosphotyrosine interaction domain proteins.. Clone UNQ421 (DNA41404-1352) has been deposited with ATCC and is assigned ATCC deposit no. 209844.

EXAMPLE 35: Isolation of cDNA Clones Encoding Human PRO846

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA39949. Based on the DNA39949 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO846.

Forward and reverse PCR primers were synthesized:

forward PCR primer 5'-CCCTGCAGTGCACCTACAGGGAAG-3' (SEQ ID NO:217)

reverse PCR primer 5'-CTGTCTTCCCCTGCTTGGCTGTGG-3' (SEQ ID NO:218)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA39949 sequence which had the following nucleotide sequence

hybridization probe

5'-GGTGCAGGAAGGGTGGGATCCTCTTCTCTCGCTGCTCTGGCCACATC-3'

(SEQ ID NO:219)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO846 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO846 [herein designated as UNQ422 (DNA44196-1353)] (SEQ ID NO:215) and the derived protein sequence for PRO846.

The entire nucleotide sequence of UNQ422 (DNA44196-1353) is shown in Figure 78 (SEQ ID NO:215). Clone UNQ422 (DNA44196-1353) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 25-27 and ending at the stop codon at nucleotide positions 1021-1023

(Figure 78). The predicted polypeptide precursor is 332 amino acids long (Figure 79). The full-length PRO846 protein shown in Figure 79 has an estimated molecular weight of about 36,143 daltons and a pI of about 5.89. Important regions of the amino acid sequence of PRO846 include the signal peptide, the transmembrane domain, an N-glycosylation site, a sequence typical of fibrinogen beta and gamma chains C-terminal domain, and a sequence typical of Ig like V-type domain as shown in Figure 79. Clone UNQ422 (DNA44196-1353) has been deposited with ATCC and is assigned ATCC deposit no. 209847.

EXAMPLE 36: Isolation of cDNA Clones Encoding Human PRO862

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA47370. Based on the DNA47370 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO862.

Forward and reverse PCR primers were synthesized:

forward PCR primer 5'GGGATCATGTTGTTGGCCCTGGTC-3' (SEQ ID NO:222)

reverse PCR primer 5'-GCAAGGCAGACCCAGTCAGCCAG-3' (SEQ ID NO:223)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA47370 sequence which had the following nucleotide sequence

hybridization probe

5'-CTGCCTGCTACCCTCCAAGTGAGGCCAAGCTCTACGGTCGTTGTG-3' (SEQ ID NO:225)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO862 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human pancreas tissue (LIB55).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO862 [herein designated as UNQ424 (DNA52187-1354)] (SEQ ID NO:220) and the derived protein sequence for PRO862.

The entire nucleotide sequence of UNQ424 (DNA52187-1354) is shown in Figure 80 (SEQ ID NO:220). Clone UNQ424 (DNA52187-1354) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 410-412 and ending at the stop codon at nucleotide positions 848-850 (Figure 80). The predicted polypeptide precursor is 146 amino acids long (Figure 81). The full-length PRO862 protein shown in Figure 81 has an estimated molecular weight of about 16,430 daltons and a pI of about 5.05. Important regions of the amino acid sequence of PRO862 include the signal peptide, an N-myristoylation site, and sequences having similarity to region to Alpha-lactalbumin/lysozyme C proteins as shown in Figure 81. Clone UNQ424 (DNA52187-1354) has been deposited with the ATCC and is assigned ATCC deposit no. 209845.

EXAMPLE 37: Isolation of cDNA Clones Encoding Human PRO864

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA40666. Based on the DNA40666 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO864.

Forward and reverse PCR primers were synthesized:

forward PCR primer 5'-GCTGCAGCTGCAAATTCCACTGG-3' (SEQ ID NO:227)

reverse PCR primer 5'-TGGTGGGAGACTGTTTAAATTATCGGCC-3' (SEQ ID NO:228)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA40666 sequence which had the following nucleotide sequence

hybridization probe

5'-TGCTTCGTCAAGTGCCGGCAGTGCCAGCGGCTCGTGGAGTT-3'

(SEQ ID NO:229)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO864 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal brain tissue (LIB153).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO864 [herein designated as UNQ426 (DNA48328-1355)] (SEQ ID NO:225) and the derived protein sequence for PRO864.

The entire nucleotide sequence of UNQ426 (DNA48328-1355) is shown in Figure 82 (SEQ ID NO:225). Clone UNQ426 (DNA48328-1355) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 37-39 and ending at the stop codon at nucleotide positions 1090-1092 (Figure 82). The predicted polypeptide precursor is 351 amino acids long (Figure 83). The full-length PRO864 protein shown in Figure 83 has an estimated molecular weight of about 39,052 and a pI of about 8.97. Important regions of the amino acid sequence of PRO864 include the signal peptide, two N-glycosylation sites, a Wnt-1 family signature sequence, and sequence regions homologous to Wnt-1 family proteins as shown in Figure 83. Clone UNQ426 (DNA48328-1355) has been deposited with ATCC and is assigned ATCC deposit no. 209843.

EXAMPLE 38: Isolation of cDNA Clones Encoding Human PRO792

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA38106. Based on the DNA38106 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO792.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GCGAGAACTGTGTCATGATGCTGC-3' (SEQ ID NO:232)

reverse PCR primer 5'-GTTTCTGAGACTCAGCAGCGGTGG-3' (SEQ ID NO:233)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA38106 sequence which had the following nucleotide sequence

hybridization probe

5'-CACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAGAAAAGGCACAAC-3' (SEQ ID NO:234)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO792 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human bone marrow tissue (LIB255).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO792 [herein designated as UNQ431 (DNA56352-1358)] (SEQ ID NO:230) and the derived protein sequence for PRO792.

The entire nucleotide sequence of UNQ431 (DNA56352-1358) is shown in Figure 84 (SEQ ID NO:230). Clone UNQ431 (DNA56352-1358) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 67-69 and ending at the stop codon at nucleotide positions 946-948 (Figure 84). The predicted polypeptide precursor is 293 amino acids long (Figure 85). The full-length PRO792 protein shown in Figure 85 has an estimated molecular weight of about 32,562 daltons and a pI of about 6.53. Analysis of the full-length PRO792 sequence shown in Figure 85 (SEQ ID NO:231) evidences the presence of the following: a type II transmembrane domain from about amino acid 31 to about amino acid 54, potential N-glycosylation sites from about amino acid 73 to about amino acid 76 and from about amino acid 159 to about amino acid 162, a leucine zipper amino acid sequence pattern from about amino acid 102 to about amino acid 123, potential N-myristolation sites from about amino acid 18 to about amino acid 23, from about amino acid 133 to about amino acid 138 and from about amino acid 242 to about amino acid 247 and a C-type lectin domain signature block from about amino acid 264 to about amino acid 287. Clone UNQ431 (DNA56352-1358) has been deposited with ATCC on May 6, 1998 and is assigned ATCC deposit no. 209846.

Analysis of the amino acid sequence of the full-length PRO792 polypeptide suggests that it possesses significant sequence similarity to the CD23 protein, thereby indicating that PRO792 may be a novel CD23 homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO792 amino acid sequence and the following Dayhoff sequences, S34198, A07100_1, A05303_1, P_R41689, P_P82839, A10871_1, P_R12796, P_R47199, A46274 and P_R32188.

EXAMPLE 39: Isolation of cDNA Clones Encoding Human PRO866

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA44708. Based on the DNA44708 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for

PRO866.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 5'-CAGCACTGCCAGGGGAAGAGGG-3' (SEQ ID NO:237)

forward PCR primer 2 5'-CAGGACTCGCTACGTCCG-3' (SEQ ID NO:238)

forward PCR primer 3 5'-CAGCCCCTTCTCCTCCTTTCTCCC-3' (SEQ ID NO:239)

reverse PCR primer 1 5'-GCAGTTATCAGGGACGCACTCAGCC-3' (SEQ ID NO:240)

reverse PCR primer 2 5'-CCAGCGAGAGGCAGATAG-3' (SEQ ID NO:241)

reverse PCR primer 3 5'-CGGTCACCGTGTCCTGCGGGATG-3' (SEQ ID NO:242)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA44708 sequence which had the following nucleotide sequence

hybridization probe

5'-CAGCCCCTTCTCCTCCTTTCTCCCACGTCCTATCTGCCTCTC-3' (SEQ ID NO:243)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO866 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB228).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO866 [herein designated as UNQ435 (DNA53971-1359)] (SEQ ID NO:235) and the derived protein sequence for PRO866.

The entire nucleotide sequence of UNQ435 (DNA53971-1359) is shown in Figure 86 (SEQ ID NO:235). Clone UNQ435 (DNA53971-1359) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 275-277 and ending at the stop codon at nucleotide positions 1268-1270 (Figure 86). The predicted polypeptide precursor is 331 amino acids long (Figure 87). The full-length PRO866 protein shown in Figure 87 has an estimated molecular weight of about 35,844 daltons and a pI of about 5.45. Analysis of the full-length PRO866 sequence shown in Figure 87 (SEQ ID NO:236) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 26. Clone UNQ435 (DNA53971-1359) has been deposited with ATCC on April 7, 1998 and is assigned ATCC deposit no. 209750.

Analysis of the amino acid sequence of the full-length PRO866 polypeptide suggests that it possesses significant sequence similarity to the mindin/spondin family of proteins, thereby indicating that PRO866 may be a novel mindin homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO866 amino acid sequence and the following Dayhoff sequences, AB006085_1, AB006084_1, AB006086_1, AF017267_1, CWU42213_1, AC004160_1, CPMICRP_1, S49108, A48569 and I46687.

EXAMPLE 40: Isolation of cDNA Clones Encoding Human PRO871

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA40324. Based on the DNA40324

consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO871.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 5'-TGCGGAGATCCTACTGGCACAGGG-3' (SEQ ID NO:246)

forward PCR primer 2 5'-CGAGTTAGTCAGAGCATG-3' (SEQ ID NO:247)

forward PCR primer 3 5'-CAGATGGTGCTGTTGCCG-3' (SEQ ID NO:248)

reverse PCR primer 1 5'-CAACTGGAACAGGAACTGAGATGTGGATC-3' (SEQ ID NO:249)

reverse PCR primer 2 5'-CTGGTTCAGCAGTGCAAGGGTCTG-3' (SEQ ID NO:250)

reverse PCR primer 3 5'-CCTCTCCGATTAAAACGC-3' (SEQ ID NO:251)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA40324 sequence which had the following nucleotide sequence

hybridization probe

5'-GAGAGGACTGGTTGCCATGGCAAATGCTGGTTCTCATGATAATGG-3' (SEQ ID NO:252)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO871 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO871 [herein designated as UNQ438 (DNA50919-1361)] (SEQ ID NO:244) and the derived protein sequence for PRO871.

The entire nucleotide sequence of UNQ438 (DNA50919-1361) is shown in Figure 88 (SEQ ID NO:244). Clone UNQ438 (DNA50919-1361) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 191-193 and ending at the stop codon at nucleotide positions 1607-1609 (Figure 88). The predicted polypeptide precursor is 472 amino acids long (Figure 89). The full-length PRO871 protein shown in Figure 89 has an estimated molecular weight of about 53,847 daltons and a pI of about 5.75. Analysis of the full-length PRO871 sequence shown in Figure 89 (SEQ ID NO:245) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 21, potential N-glycosylation sites from about amino acid 109 to about amino acid 112 and from about amino acid 201 to about amino acid 204, a cyclophilin-type peptidy-prolyl cis-trans isomerase signature sequence from about amino acid 49 to about amino acid 66 and regions that are homologous to cyclophilin-type peptidy-prolyl cis-trans isomerases from about amino acid 96 to about amino acid 140, from about amino acid 49 to about amino acid 89 and from about amino acid 22 to about amino acid 51. Clone UNQ438 (DNA50919-1361) has been deposited with ATCC on May 6, 1998 and is assigned ATCC deposit no. 209848.

Analysis of the amino acid sequence of the full-length PRO871 polypeptide suggests that it possesses significant sequence similarity to the cyclophilin family of proteins, thereby indicating that PRO871 may be a novel cyclophilin protein family member. More specifically, an analysis of the Dayhoff database (version 35.45

SwissProt 35) evidenced significant homology between the PRO871 amino acid sequence and the following Dayhoff sequences, SPBC16H5_5, S64705, YAL5_SCHPO, CYP4_CAEEL, CELC34D4_7, CYPA_CAEEL, HUMORF006_1, CYPI_MYCTU, AF043642_1 and HSSRCYP_1.

EXAMPLE 41: Isolation of cDNA Clones Encoding Human PRO873

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA39621. Based on the DNA39621 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO873.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-AGGTGCCTGCAGGAGTCCTGGGG-3' (SEQ ID NO:255)

reverse PCR primer 5'- CCACCTCAGGAAGCCGAAGATGCC-3' (SEQ ID NO:256)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA39621 sequence which had the following nucleotide sequence:

hybridization probe

5'-GAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCTG-3' (SEQ ID NO:257)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO873 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal liver tissue (LIB229).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO873 [herein designated as UNQ440 (DNA44179-1362)] (SEQ ID NO:253) and the derived protein sequence for PRO873.

The entire nucleotide sequence of UNQ440 (DNA44179-1362) is shown in Figure 90 (SEQ ID NO:253). Clone UNQ440 (DNA44179-1362) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 139-141 and ending at the stop codon at nucleotide positions 1774-1776 (Figure 90). The predicted polypeptide precursor is 545 amino acids long (Figure 91). The full-length PRO873 protein shown in Figure 91 has an estimated molecular weight of about 58,934 daltons and a pI of about 9.45. Analysis of the full-length PRO873 sequence shown in Figure 91 (SEQ ID NO:254) evidences the presence of the following features: a signal peptide from about amino acid 1 to about amino acid 29; a carboxylesterase type-B serine active site at about amino acid 312 to about amino acid 327; a carboxylesterase type-B signature 2 motif at about amino acid 218 to about amino acid 228; and three potential N-glycosylation sites at about amino acid 318 to about amino acid 321, about amino acid 380 to about amino acid 383, and about amino acid 465 to about amino acid 468. Clone UNQ440 (DNA44179-1362) has been deposited with ATCC on May 6, 1998 and is assigned ATCC deposit no. 209851.

Analysis of the amino acid sequence of the full-length PRO873 polypeptide suggests that it possesses

significant sequence similarity to a human liver carboxylesterase, thereby indicating that PRO873 may be a novel carboxylesterase. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO873 amino acid sequence and the following Dayhoff sequences: ES10_RAT, GEN12405, AB010633_1, EST4_RAT, A48809, SASB_ANAPL, RNU41662_1, RNU22952_1, BAL_RAT, GEN13522.

EXAMPLE 42: Isolation of cDNA Clones Encoding Human PRO940

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA47442. Based on the DNA47442 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO940.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CAAAGCCTGCGCCTGGTCTGTG-3' (SEQ ID NO:260)

reverse PCR primer 5'-TTCTGGAGCCCAGAGGGTGCTGAG-3' (SEQ ID NO:262)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA47442 sequence which had the following nucleotide sequence

hybridization probe

5'-GGAGCTGCCACCCATTCAAATGGAGCACGAAGGAGAGTTCACCTG-3' (SEQ ID NO:263)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO940 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal liver tissue (LIB229).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO940 [herein designated as UNQ477 (DNA54002-1367)] (SEQ ID NO:258) and the derived protein sequence for PRO940.

The entire nucleotide sequence of UNQ477 (DNA54002-1367) is shown in Figure 92 (SEQ ID NO:258). Clone UNQ477 (DNA54002-1367) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 46-48 and ending at the stop codon at nucleotide positions 1678-1680 (Figure 92). The predicted polypeptide precursor is 544 amino acids long (Figure 93). The full-length PRO940 protein shown in Figure 93 has an estimated molecular weight of about 60,268 daltons and a pI of about 9.53. Analysis of the full-length PRO940 sequence shown in Figure 93 (SEQ ID NO:259) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 15, potential N-glycosylation sites from about amino acid 100 to about amino acid 103, from about amino acid 297 to about amino acid 300 and from about amino acid 306 to about amino acid 309 and an immunoglobulin and major histocompatibility complex signature sequence block from about amino acid 365 to about amino acid 371. Clone UNQ477 (DNA54002-1367) has been deposited with ATCC on April 7, 1998 and is assigned ATCC deposit no. 209754.

Analysis of the amino acid sequence of the full-length PRO940 polypeptide suggests that it possesses significant sequence similarity to CD33 and the OB binding protein-2. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO940 amino acid sequence and the following Dayhoff sequences, CD33_HUMAN, HSU71382_1, HSU71383_1, D86359_1, PGBM_HUMAN, MAGS_MOUSE, D86983_1, C22B_HUMAN, P_W01002 and HVU24116_1.

EXAMPLE 43: Isolation of cDNA Clones Encoding Human PRO941

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA35941. An EST sequence proprietary to Genentech was employed in the assembly and is herein designated DNA6415 (Figure 96; SEQ ID NO:265). Based on the DNA35941 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO941.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CTTGACTGTCTCTGAATCTGCACCC-3' (SEQ ID NO:266)

reverse PCR primer 5'-AAGTGGTGGAAGCCTCCAGTGTGG-3' (SEQ ID NO:267)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35941 sequence which had the following nucleotide sequence

hybridization probe

5'-CCACTACGGTATTAGAGCAAAAGTTAAAAACCATCATGGTTCCTGGAGCAGC-3' (SEQ ID NO:268)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO941 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO941 [herein designated as UNQ478 (DNA53906-1368)] (SEQ ID NO:263) and the derived protein sequence for PRO941.

The entire nucleotide sequence of UNQ478 (DNA53906-1368) is shown in Figure 94 (SEQ ID NO:263). Clone UNQ478 (DNA53906-1368) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 37-39 and ending at the stop codon at nucleotide positions 2353-2355 (Figure 94). The predicted polypeptide precursor is 772 amino acids long (Figure 95). The full-length PRO941 protein shown in Figure 95 has an estimated molecular weight of about 87,002 daltons and a pI of about 4.64. Analysis of the full-length PRO941 sequence shown in Figure 95 (SEQ ID NO:264) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 21, potential N-glycosylation sites from about amino acid 57 to about amino acid 60, from about amino acid 74 to about amino acid 77, from about amino acid 419 to about amino acid 422, from about amino acid 437 to about amino acid 440, from about amino acid 508 to about amino acid 511, from about amino acid 515 to about amino acid 518, from about amino acid

516 to about amino acid 519 and from about amino acid 534 to about amino acid 537, and cadherin extracellular repeated domain signature sequences from about amino acid 136 to about amino acid 146 and from about amino acid 244 to about amino acid 254. Clone UNQ478 (DNA53906-1368) has been deposited with ATCC on April 7, 1998 and is assigned ATCC deposit no. 209747.

Analysis of the amino acid sequence of the full-length PRO941 polypeptide suggests that it possesses significant sequence similarity to a cadherin protein, thereby indicating that PRO941 may be a novel cadherin protein family member. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO941 amino acid sequence and the following Dayhoff sequences, I50180, CADA_CHICK, I50178, GEN12782, CADC_HUMAN, P_W25637, A38992, P_R49731, D38992 and G02678.

EXAMPLE 44: Isolation of cDNA Clones Encoding Human PRO944

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA47374. A variety of proprietary Genentech EST sequences were employed in the assembly and are shown in Figures 99-107. Based on the DNA47374 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO944.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CGAGCGAGTCATGGCCAACGC-3' (SEQ ID NO:280)

reverse PCR primer 5'-GTGTCACACGTAGTCTTTCCCGCTGG-3' (SEQ ID NO:281)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA47374 sequence which had the following nucleotide sequence

hybridization probe

5'-CTGCAGCTGTTGGGCTTCATTCTCGCCTTCCTGGGATGGATCG-3' (SEQ ID NO:282)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO944 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO944 [herein designated as UNQ481 (DNA52185-1370)] (SEQ ID NO:269) and the derived protein sequence for PRO944.

The entire nucleotide sequence of UNQ481 (DNA52185-1370) is shown in Figure 97 (SEQ ID NO:269). Clone UNQ481 (DNA52185-1370) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 219-221 and ending at the stop codon at nucleotide positions 852-854 (Figure 97). The predicted polypeptide precursor is 211 amino acids long (Figure 98). The full-length PRO944

protein shown in Figure 98 has an estimated molecular weight of about 22,744 daltons and a pI of about 8.51. Analysis of the full-length PRO944 sequence shown in Figure 98 (SEQ ID NO:270) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 21, transmembrane domains from about amino acid 82 to about amino acid 102, from about amino acid 118 to about amino acid 142 and from about amino acid 161 to about amino acid 187, a potential N-glycosylation site from about amino acid 72 to about amino acid 75, a sequence block having homology to PMP-22/EMP/MP20 family of proteins from about amino acid 70 to about amino acid 111 and a sequence block having homology to ABC-2 type transport system integral membrane protein from about amino acid 119 to about amino acid 133. Clone UNQ481 (DNA52185-1370) has been deposited with ATCC on May 14, 1998 and is assigned ATCC deposit no. 209861.

Analysis of the amino acid sequence of the full-length PRO944 polypeptide suggests that it possesses significant sequence similarity to the CPE-R protein, thereby indicating that PRO944 may be a novel CPE-R homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO944 amino acid sequence and the following Dayhoff sequences, AB000713_1, AB000714_1, AF035814_1, AF000959_1, HSU89916_1, EMP2_HUMAN, JC5732, CELF53B3_6, PM22_MOUSE and CGU49797_1.

EXAMPLE 45: Isolation of cDNA Clones Encoding Human PRO983

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA47473. Various proprietary Genentech EST sequences were employed in the assembly, wherein those EST sequences are shown in Figures 110-116. Based on the DNA47473 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO983.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GCACCACCGTAGGTACTTGTGTGAGGC-3' (SEQ ID NO:292)

reverse PCR primer 5'-AACCACCAGAGCCAAGAGCCGGG -3' (SEQ ID NO:293)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA47473 sequence which had the following nucleotide sequence

hybridization probe

5'-CAGCGGAATCATCGATGCAGGGGCCTCAATTAATGTATCTGTGATGTTAC-3' (SEQ ID NO:294)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO983 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human bone marrow (LIB256).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO983 [herein designated as UNQ484 (DNA53977-1371)] (SEQ ID NO:283) and the derived protein sequence for PRO983.

The entire nucleotide sequence of UNQ484 (DNA53977-1371) is shown in Figure 108 (SEQ ID NO:283). Clone UNQ484 (DNA53977-1371) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 234-236 and ending at the stop codon at nucleotide positions 963-965 (Figure 108). The predicted polypeptide precursor is 243 amino acids long (Figure 109). The full-length PRO983 protein shown in Figure 109 has an estimated molecular weight of about 27,228 daltons and a pI of about 7.43. Analysis of the full-length PRO983 sequence shown in Figure 109 (SEQ ID NO:284) evidences the presence of the following features: a putative transmembrane domain from about amino acid 224 to about amino acid 239; a potential N-glycosylation site from about amino acid 68 to about amino acid 71; and three potential N-myristoylation sites from about amino acid 59 to about amino acid 64, from about amino acid 64 to about amino acid 69, and from about amino acid 235 to about amino acid 240. Clone UNQ484 (DNA53977-1371) has been deposited with ATCC on May 14, 1998 and is assigned ATCC deposit no. 209862.

Analysis of the amino acid sequence of the full-length PRO983 polypeptide suggests that it possesses significant sequence similarity to the vesicle-associated protein, VAP-33, thereby indicating that PRO983 may be a novel vesicle associated membrane protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO983 amino acid sequence and the following Dayhoff sequences: VP33_APLCA, CELF33D11_12, CELF42G2_2, S50623, YDFC_SCHPO, CELF54H5_2, CELZC196_8, CEF57A10_3, MSP3_GLORO, CEC15H11_1.

EXAMPLE 46: Isolation of cDNA Clones Encoding Human PRO1057

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA49808. Based on the DNA49808 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO1057.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GCATCTGCAGGAGAGAGCGAAGGG-3' (SEQ ID NO:297)

reverse PCR primer 5'-CATCGTTCCCGTGAATCCAGAGGC-3' (SEQ ID NO:298)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA49808 sequence which had the following nucleotide sequence

hybridization probe

5'-GAAGGGAGGCCTTCCTTTCAGTGGACCCGGGTCAAGAATACCCAC-3' (SEQ ID NO:299)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO1057 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO1057 [herein designated as UNQ522 (DNA57253-1382)] (SEQ ID NO:295) and the derived protein

sequence for PRO1057.

The entire nucleotide sequence of UNQ522 (DNA57253-1382) is shown in Figure 117 (SEQ ID NO:295). Clone UNQ522 (DNA57253-1382) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 275-277 and ending at the stop codon at nucleotide positions 1514-1516 (Figure 117). The predicted polypeptide precursor is 413 amino acids long (Figure 118). The full-length PRO1057 protein shown in Figure 118 has an estimated molecular weight of about 47,070 daltons and a pI of about 9.92. Analysis of the full-length PRO1057 sequence shown in Figure 118 (SEQ ID NO:296) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 16, potential N-glycosylation sites from about amino acid 90 to about amino acid 93, from about amino acid 110 to about amino acid 113 and from about amino acid 193 to about amino acid 196, a glycosaminoglycan attachment site from about amino acid 236 to about amino acid 239 and a serine protease histidine-containing active site from about amino acid 165 to about amino acid 170. Clone UNQ522 (DNA57253-1382) has been deposited with ATCC on May 14, 1998 and is assigned ATCC deposit no. 209867.

Analysis of the amino acid sequence of the full-length PRO1057 polypeptide suggests that it possesses significant sequence similarity to various protease proteins, thereby indicating that PRO1057 may be a novel protease. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO1057 amino acid sequence and the following Dayhoff sequences,TRYE_DROER, P_R14159, A69660, EBN1_EBV, S65494, GEN12688, A51084_1, P_R99571, A57514 and AF003200_1.

EXAMPLE 47: Isolation of cDNA Clones Encoding Human PRO1071

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA53035. Based on the DNA53035 consensus sequence, it was determined that that consensus sequence shared significant sequence identity with Incyte EST clone no. 2872569, a clone that upon review appeared to encode a full length protein. As such, Incyte EST clone no. 2872569 was purchased and its insert was obtained and sequenced so as to confirm the proper sequence. This sequence is herein designated UNQ528 or DNA58847-1383.

DNA sequencing of the clone isolated as described above gave the full-length DNA sequence for PRO1071 [herein designated as UNQ528 (DNA58847-1383)] (SEQ ID NO:300) and the derived protein sequence for PRO1071.

The entire nucleotide sequence of UNQ528 (DNA58847-1383) is shown in Figure 119 (SEQ ID NO:300). Clone UNQ528 (DNA58848-1383) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 133-135 and ending at the stop codon at nucleotide positions 1708-1710 (Figure 119). The predicted polypeptide precursor is 525 amino acids long (Figure 120). The full-length PRO1071 protein shown in Figure 120 has an estimated molecular weight of about 58,416 daltons and a pI of about 6.62. Analysis of the full-length PRO1071 sequence shown in Figure 120 (SEQ ID NO:301) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 25, a potential N-

glycosylation site from about amino acid 251 to about amino acid 254, a thrombospondin-1 homology block from about amino acid 385 to about amino acid 399 and von Willibrands factor type C homology blocks from about amino acid 385 to about amino acid 399, from about amino acid 445 to about amino acid 459 and from about amino acid 42 to about amino acid 56. Clone UNQ528 (DNA58847-1383) has been deposited with ATCC on May 20, 1998 and is assigned ATCC deposit no. 209879.

Analysis of the amino acid sequence of the full-length PRO1071 polypeptide suggests that it possesses significant sequence similarity to the thrombospondin protein, thereby indicating that PRO1071 may be a novel thrombospondin homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO1071 amino acid sequence and the following Dayhoff sequences, AB002364_1, D67076_1, BTPCINPGN_1, CET13H10_1, CEF25H8_5, CEF53B6_2, CEC26C6_6, HSSEMG_1, CET21B6_4 and BTY08561_1.

EXAMPLE 48: Isolation of cDNA Clones Encoding Human PRO1072

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA53125. Based on the DNA53125 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO1072.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CCAGGAAATGCTCCAGGAAGAGCC-3' (SEQ ID NO:305)

reverse PCR primer 5'-GCCCATGACACCAAATTGAAGAGTGG-3' (SEQ ID NO:306)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA53125 sequence which had the following nucleotide sequence

hybridization probe

5'-AACGCAGGGATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGG-3' (SEQ ID NO:307)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO1072 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal lung tissue (LIB26).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO1072 [herein designated as UNQ529 (DNA58747-1384)] (SEQ ID NO:302) and the derived protein sequence for PRO1072.

The entire nucleotide sequence of UNQ529 (DNA58747-1384) is shown in Figure 121 (SEQ ID NO:302). Clone UNQ529 (DNA58747-1384) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 65-67 and ending at the stop codon at nucleotide positions 1073-1075 (Figure 121). The predicted polypeptide precursor is 336 amino acids long (Figure 122). The full-length PRO1072 protein shown in Figure 122 has an estimated molecular weight of about 36,865 daltons and a pI of

about 9.15. Analysis of the full-length PRO1072 sequence shown in Figure 122 (SEQ ID NO:303) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 21, short-chain alcohol dehydrogenase protein homology blocks from about amino acid 134 to about amino acid 144, from about amino acid 44 to about amino acid 56 and from about amino acid 239 to about amino acid 248 and potential N-glycosylation sites from about amino acid 212 to about amino acid 215 and from about amino acid 239 to about amino acid 242. Clone UNQ529 (DNA58747-1384) has been deposited with ATCC on May 14, 1998 and is assigned ATCC deposit no. 209868.

Analysis of the amino acid sequence of the full-length PRO1072 polypeptide suggests that it possesses significant sequence similarity to the reductase family of proteins, thereby indicating that PRO1072 may be a novel reductase. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO1072 amino acid sequence and the following Dayhoff sequences, P_W03198, P_W15759, P_R60800, MTV037_3, CEC15H11_6, ATAC00234314, MTV022_13, SCU43704_1, OXIR_STRAT AND CELC01G8_3.

EXAMPLE 49: Isolation of cDNA Clones Encoding Human PRO1075

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA34363. Based on the DNA34363 sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO1075.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-TGAGAGGCCTCTCTGGAAGTTG-3' (SEQ ID NO:312)

forward PCR primer 5'-GTCAGCGATCAGTGAAAGC-3' (SEQ ID NO:313)

forward PCR primer 5'-CCAGAATGAAGTAGCTCGGC-3' (SEQ ID NO:314)

forward PCR primer 5'-CCGACTCAAAATGCATTGTC-3' (SEQ ID NO:315)

forward PCR primer 5'-CATTTGGCAGGAATTGTCC-3' (SEQ ID NO:316)

forward PCR primer 5'-GGTGCTATAGGCCAAGGG-3' (SEQ ID NO:317)

reverse PCR primer 5'-CTGTATCTCTGGGCTATGTCAGAG-3' (SEQ ID NO:318)

reverse PCR primer 5'-CTACATATAATGGCACATGTCAGCC-3' (SEQ ID NO:319)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA34363 sequence which had the following nucleotide sequence

hybridization probe

5'-CGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTG-3' (SEQ ID NO:320)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO1075 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human skin tumor tissue (LIB324).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO1075 [herein designated as UNQ532 (DNA57689-1385)] (SEQ ID NO:308) and the derived protein sequence for PRO1075.

The entire nucleotide sequence of UNQ532 (DNA57689-1385) is shown in Figure 124 (SEQ ID NO:308). Clone UNQ532 (DNA57689-1385) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 137-139 and ending at the stop codon at nucleotide positions 1355-1357 (Figure 124). The predicted polypeptide precursor is 406 amino acids long (Figure 125). The full-length PRO1075 protein shown in Figure 125 has an estimated molecular weight of about 46,927 daltons and a pI of about 5.21. Analysis of the full-length PRO1075 sequence shown in Figure 125 (SEQ ID NO:309) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 29, an endoplasmic reticulum targeting sequence from about amino acid 403 to about amino acid 406, a tyrosine kinase phosphorylation site from about amino acid 203 to about amino acid 211 and a sequence block having homology to the thioredoxin family of proteins from about amino acid 50 to about amino acid 66. Clone UNQ532 (DNA57689-1385) has been deposited with ATCC on May 14, 1998 and is assigned ATCC deposit no. 209869.

Analysis of the amino acid sequence of the full-length PRO1075 polypeptide suggests that it possesses significant sequence similarity to protein disulfide isomerase, thereby indicating that PRO1075 may be a novel protein disulfide isomerase. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO1075 amino acid sequence and the following Dayhoff sequences, CELC30H7_2, CELC06A6_3, CELF42G8_3, S57942, ER72_CAEEL, CELC07A12_3, CEH06O01_4 and P_R51696.

EXAMPLE 50: Isolation of cDNA Clones Encoding Human PRO181

A cDNA sequence isolated in the amylase screen described in Example 2 above was found, by BLAST and FastA sequence alignment, to have sequence homology to a nucleotide sequence encoding the cornichon protein. This cDNA sequence is herein designated DNA13242 (Figure 130; SEQ ID NO:323). Based on the sequence homology, oligonucleotide probes were generated from the sequence of the DNA13242 molecule and used to screen a human placenta (LIB89) library prepared as described in paragraph 1 of Example 2 above. The cloning vector was pRK5B (pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)), and the cDNA size cut was less than 2800 bp.

The oligonucleotide probes employed included:

forward PCR primer 5'-GTGCAGCAGAGTGGCTTACA-3' (SEQ ID NO:326)

reverse PCR primer 5'-ACTGGACCAATTCTTCTGTG-3' (SEQ ID NO:327)

hybridization probe

5'-GATATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCT-3' (SEQ ID NO:328)

A full length clone was identified that contained a single open reading frame with an apparent translational initiation site at nucleotide positions 14-16 and ending at the stop codon found at nucleotide positions 446-448 (Figure 128; SEQ ID NO:321). The predicted polypeptide precursor is 144 amino acids long, has a

calculated molecular weight of approximately 16,699 daltons and an estimated pI of approximately 5.6. Analysis of the full-length PRO181 sequence shown in Figure 129 (SEQ ID NO:322) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 20, a putative type II transmembrane domain from about amino acid 11 to about amino acid 31 and other transmembrane domains from about amino acid 57 to about amino acid 77 and from about amino acid 123 to about amino acid 143. Clone UNQ155 (DNA23330-1390) has been deposited with ATCC on April 14, 1998 and is assigned ATCC deposit no. 209775.

Analysis of the amino acid sequence of the full-length PRO181 polypeptide suggests that it possesses significant sequence similarity to the cornichon protein, thereby indicating that PRO181 may be a novel cornichon homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO181 amino acid sequence and the following Dayhoff sequences, AF022811_1, CET09E8_3, S64058, YGF4_YEAST, YB60_YEAST, EBU89455_1, SIU36383_3 and PH1371.

EXAMPLE 51: Isolation of cDNA Clones Encoding Human PRO195

A cDNA sequence was isolated in the amylase screen described in Example 2 above and is herein designated DNA13199 (Figure 134; SEQ ID NO:332). The DNA13199 sequence was then compared to a variety of expressed sequence tag (EST) databases which included public EST databases (e.g., GenBank) to identify existing homologies. The homology search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Washington; http://bozeman.mbt.washington.edu/phrap.docs/phrap.html). The consensus sequence obtained therefrom is herein designated as DNA22778.

Based on the DNA22778 sequence, oligonucleotide probes were generated and used to screen a human placenta library (LIB89) prepared as described in paragraph 1 of Example 2 above. The cloning vector was pRK5B (pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)), and the cDNA size cut was less than 2800 bp.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-ACAAGCTGAGCTGCTGTGACAG-3' (SEQ ID NO:333)

reverse PCR primer 5'-TGATTCTGGCAACCAAGATGGC-3' (SEQ ID NO:334)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA22778 sequence which had the following nucleotide sequence

hybridization probe

5'-ATGGCCTTGGCCGGAGGTTCGGGGACCGCTTCGGCTGAAG-3' (SEQ ID NO:335)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO195 gene using the probe oligonucleotide and one of the PCR primers.

A full length clone was identified that contained a single open reading frame with an apparent

translational initiation site at nucleotide positions 70-72 and ending at the stop codon found at nucleotide positions 1039-1041 (Figure 132; SEQ ID NO:330). The predicted polypeptide precursor is 323 amino acids long, has a calculated molecular weight of approximately 36,223 daltons and an estimated pI of approximately 5.06. Analysis of the full-length PRO195 sequence shown in Figure 132 (SEQ ID NO:330) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 31, a transmembrane domain from about amino acid 241 to about amino acid 260 and a potential N-glycosylation site from about amino acid 90 to about amino acid 93. Clone UNQ169 (DNA26847-1395) has been deposited with ATCC on April 14, 1998 and is assigned ATCC deposit no. 209772.

Analysis of the amino acid sequence of the full-length PRO195 polypeptide suggests that it possesses no significant sequence similarity to any known protein. However, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced some degree of homology between the PRO195 amino acid sequence and the following Dayhoff sequences, P_P91380, AF035118_1, HUMTROPCS_1, NUOD_SALTY and E70002.

EXAMPLE 52: Isolation of cDNA Clones Encoding Human PRO865

A cDNA sequence isolated in the amylase screen described in Example 2 above was herein designated DNA37642 (Figure 137, SEQ ID NO:338). The DNA37642 sequence was then compared to a variety of expressed sequence tag (EST) databases which included public EST databases (e.g., GenBank) and a proprietary EST DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA) to identify homologies therebetween. The homology search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Washington; http://bozeman.mbt.washington.edu/phrap.docs/phrap.html). The consensus sequence obtained is herein designated DNA48615.

Based on the DNA48615 consensus sequence, probes were generated and used to screen a human fetal kidney (LIB227) library prepared as described in paragraph 1 of Example 2 above. The cloning vector was pRK5B (pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)), and the cDNA size cut was less than 2800 bp.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 5'-AAGCTGCCGGAGCTGCAATG-3' (SEQ ID NO:339)
forward PCR primer 2 5'-TTGCTTCTTAATCCTGAGCGC-3' (SEQ ID NO:340)
forward PCR primer 3 5'-AAAGGAGGACTTTCGACTGC-3' (SEQ ID NO:341)
reverse PCR primer 1 5'-AGAGATTCATCCACTGCTCCAAGTCG-3' (SEQ ID NO:342)
reverse PCR primer 2 5'-TGTCCAGAAACAGGCACATATCAGC-3' (SEQ ID NO:343)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA48615 sequence which had the following nucleotide sequence

hybridization probe

5'-AGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGAT-3' (SEQ ID NO:344)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO865 gene using the probe oligonucleotide and one of the PCR primers.

A full length clone was identified that contained a single open reading frame with an apparent translational initiation site at nucleotide positions 173-175 and ending at the stop codon found at nucleotide positions 1577-1579 (Figure 135; SEQ ID NO:336). The predicted polypeptide precursor is 468 amino acids long, has a calculated molecular weight of approximately 54,393 daltons and an estimated pI of approximately 5.63. Analysis of the full-length PRO865 sequence shown in Figure 136 (SEQ ID NO:337) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 23, potential N-glycosylation sites from about amino acid 280 to about amino acid 283 and from about amino acid 384 to about amino acid 387, a potential amidation site from about amino acid 94 to about amino acid 97, glycosaminoglycan attachment sites from about amino acid 20 to about amino acid 23 and from about amino acid 223 to about amino acid 226, an aminotransferase class-V pyridoxyl-phosphate amino acid sequence block from about amino acid 216 to about amino acid 222 and an amino acid sequence block similar to that found in the interleukin-7 protein from about amino acid 338 to about amino acid 343. Clone UNQ434 (DNA53974-1401) has been deposited with ATCC on April 14, 1998 and is assigned ATCC deposit no. 209774.

Analysis of the amino acid sequence of the full-length PRO865 polypeptide suggests that it possesses no significant sequence similarity to any known protein. However, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced some degree of homology between the PRO865 amino acid sequence and the following Dayhoff sequences, YMN0_YEAST, ATFCA4_43, S44168, P_W14549 and RABTCRG4_1.

EXAMPLE 53: Isolation of cDNA Clones Encoding Human PRO827

A cDNA sequence isolated in the amylase screen described in Example 2 above was found, by BLAST and FastA sequence alignment, to have sequence homology to nucleotide sequences encoding various integrin proteins. This cDNA sequence is herein designated DNA47751 (see Figure 140; SEQ ID NO:347). Based on the sequence homology, probes were generated from the sequence of the DNA47751 molecule and used to screen a human fetal pigment epithelium library (LIB113) prepared as described in paragraph 1 of Example 2 above. The cloning vector was pRK5B (pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)), and the cDNA size cut was less than 2800 bp.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-AGGGACAGAGGCCAGAGGACTTC-3' (SEQ ID NO:348)

reverse PCR primer 5'-CAGGTGCATATTCACAGCAGGATG-3' (SEQ ID NO:349)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA47751 sequence which had the following nucleotide sequence

hybridization probe

5'-GGAACTCCCCTTCGTCACTCACCTGTTCTTGCCCCTGGTGTTCCT-3' (SEQ ID

NO:350)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO827 gene using the probe oligonucleotide and one of the PCR primers.

A full length clone was identified that contained a single open reading frame with an apparent translational initiation site at nucleotide positions 134-136 and ending at the stop codon found at nucleotide positions 506-508 (Figure 138; SEQ ID NO:345). The predicted polypeptide precursor is 124 amino acids long, has a calculated molecular weight of approximately 13,352 daltons and an estimated pI of approximately 5.99. Analysis of the full-length PRO827 sequence shown in Figure 139 (SEQ ID NO:346) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 22, a cell attachment sequence from about amino acid 70 to about amino acid 72, a potential N-glycosylation site from about amino acid 98 to about amino acid 101 and an integrin alpha chain protein homology sequence from about amino acid 67 to about amino acid 81. Clone UNQ468 (DNA57039-1402) has been deposited with ATCC on April 14, 1998 and is assigned ATCC deposit no. 209777.

Analysis of the amino acid sequence of the full-length PRO827 polypeptide suggests that it possesses significant sequence similarity to the VLA-2 integrin protein and various other integrin proteins, thereby indicating that PRO827 may be a novel integrin or splice variant thereof. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO240 amino acid sequence and the following Dayhoff sequences, S44142, ITA2_HUMAN, ITA1_RAT, ITA1_HUMAN, ITA4_HUMAN, ITA9_HUMAN, AF032108_1, ITAM_MOUSE, ITA8_CHICK and ITA6_CHICK.

EXAMPLE 54: Isolation of cDNA Clones Encoding Human PRO1114

A cDNA sequence isolated in the amylase screen described in Example 2 was found, by the WU-BLAST2 sequence alignment computer program, to have certain sequence identity to other known interferon receptors. This cDNA sequence is herein designated DNA48466 (Figure 143; SEQ ID NO:352). Based on the sequence identity, probes were generated from the sequence of the DNA48466 molecule and used to screen a human breast carconoma library (LIB135) prepared as described in paragraph 1 of Example 2 above. The cloning vector was pRK5B (pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)), and the cDNA size cut was less than 2800 bp.

The oligonucleotide probes employed were as follows:

forward PCR primer 5'-AGGCTTCGCTGCGACTAGACCTC-3' (SEQ ID NO:354)

reverse PCR primer 5'-CCAGGTCGGGTAAGGATGGTTGAG-3' (SEQ ID NO:355)

hybridization probe

5'-TTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC-3' (SEQ ID NO:356)

A full length clone was identified that contained a single open reading frame with an apparent translational initiation site at nucleotide positions 250-252, and a stop signal at nucleotide positions 1183-1185 (Figure 141, SEQ ID NO:351). The predicted polypeptide precursor is 311 amino acids long, has a calculated

molecular weight of approximately 35,076 daltons and an estimated pI of approximately 5.04. Analysis of the full-length PRO1114 interferon receptor sequence shown in Figure 142 (SEQ ID NO:352) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 29, a transmembrane domain from about amino acid 230 to about amino acid 255, potential N-glycosylation sites from about amino acid 40 to about amino acid 43 and from about amino acid 134 to about amino acid 137, an amino acid sequence block having homology to tissue factor proteins from about amino acid 92 to about amino acid 119 and an amino acid sequence block having homology to integrin alpha chain proteins from about amino acid 232 to about amino acid 262. Clone UNQ557 (DNA57033-1403) has been deposited with ATCC on May 27, 1998 and is assigned ATCC deposit no. 209905.

An analysis of the Dayhoff database (version 35.45 SwissProt 35), using a WU-BLAST2 sequence alignment analysis of the full-length sequence shown in Figure 142 (SEQ ID NO:352), evidenced significant homology between the PRO1114 interferon receptor amino acid sequence and the following Dayhoff sequences: G01418, INR1_MOUSE, P_R71035, INGS_HUMAN, A26595_1, A26593_1, I56215 and TF_HUMAN.

EXAMPLE 55: Isolation of cDNA Clones Encoding Human PRO237

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA30905. Based on the DNA30905 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO237.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-TCTGCTGAGGTGCAGCTCATTCAC-3' (SEQ ID NO:359)

reverse PCR primer 5'-GAGGCTCTGGAAGATCTGAGATGG-3' (SEQ ID NO:360)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30905 sequence which had the following nucleotide sequence

hybridization probe

5'-GCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCATTCCTCAGTCGCCTC-3' (SEQ ID NO:361)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO237 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal brain tissue (LIB153).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO237 [herein designated as UNQ211 (DNA34353-1428)] (SEQ ID NO:357) and the derived protein sequence for PRO237.

The entire nucleotide sequence of UNQ211 (DNA34353-1428) is shown in Figure 144 (SEQ ID NO:357). Clone UNQ211 (DNA34353-1428) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 586-588 and ending at the stop codon at nucleotide positions 1570-1572

(Figure 144). The predicted polypeptide precursor is 328 amino acids long (Figure 145). The full-length PRO237 protein shown in Figure 145 has an estimated molecular weight of about 36,238 daltons and a pI of about 9.90. Analysis of the full-length PRO237 sequence shown in Figure 145 (SEQ ID NO:358) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 23, a transmembrane domain from about amino acid 177 to about amino acid 199, potential N-glycosylation sites from about amino acid 118 to about amino acid 121, from about amino acid 170 to about amino acid 173 and from about amino acid 260 to about amino acid 263 and eukaryotic-type carbonic anhydrase sequence homology blocks from about amino acid 222 to about amino acid 270, from about amino acid 128 to about amino acid 164 and from about amino acid 45 to about amino acid 92. Clone UNQ211 (DNA34353-1428) has been deposited with ATCC on May 12, 1998 and is assigned ATCC deposit no. 209855.

Analysis of the amino acid sequence of the full-length PRO237 polypeptide suggests that it possesses significant sequence similarity to the carbonic anhydrase protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO237 amino acid sequence and the following Dayhoff sequences, AF050106_1, OACALP_1, CELD1022_8, CAH2_HUMAN, 1CAC, CAH5_HUMAN, CAHP_HUMAN, CAH3_HUMAN, CAH1_HUMAN and 2CAB.

EXAMPLE 56: Isolation of cDNA Clones Encoding Human PRO541

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA42259. Based on the DNA42259 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO541.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GGACAGAATTTGGGAGCACACTGG-3' (SEQ ID NO:364)

forward PCR primer 5'-CCAAGAGTATACTGTCCTCG-3' (SEQ ID NO:365)

reverse PCR primer 5'-AGCACAGATTTTCTCTACAGCCCCC-3' (SEQ ID NO:366)

reverse PCR primer 5'-AACCACTCCAGCATGTACTGCTGC-3' (SEQ ID NO:367)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA42259 sequence which had the following nucleotide sequence

hybridization probe

5'-CCATTCAGGTGTTCTGGCCCTGTATGTACACATTATACACAGGTCGTGTG-3' (SEQ ID NO:368)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO541 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO541 [herein designated as UNQ342 (DNA45417-1432)] (SEQ ID NO:362) and the derived protein sequence

for PRO541.

The entire nucleotide sequence of UNQ342 (DNA45417-1432) is shown in Figure 146 (SEQ ID NO:362). Clone UNQ342 (DNA45417-1432) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 469-471 and ending at the stop codon at nucleotide positions 1969-1971 (Figure 146). The predicted polypeptide precursor is 500 amino acids long (Figure 147). The full-length PRO541 protein shown in Figure 147 has an estimated molecular weight of about 56,888 daltons and a pI of about 8.53. Analysis of the full-length PRO541 sequence shown in Figure 147 (SEQ ID NO:363) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 20, amino acid sequence blocks having homology to extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 from about amino acid 165 to about amino acid 186, from about amino acid 196 to about amino acid 218, from about amino acid 134 to about amino acid 146, from about amino acid 96 to about amino acid 108 and from about amino acid 58 to about amino acid 77 and a potential N-glycosylation site from about amino acid 28 to about amino acid 31. Clone UNQ342 (DNA45417-1432) has been deposited with ATCC on May 27, 1998 and is assigned ATCC deposit no. 209910.

Analysis of the amino acid sequence of the full-length PRO541 polypeptide suggests that it possesses significant sequence similarity to a trypsin inhibitor protein, thereby indicating that PRO541 may be a novel trypsin inhibitor. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO541 amino acid sequence and the following Dayhoff sequences, D45027_1, AB009609_1, JC5308, CRS3_HORSE, TPX1_HUMAN, HELO_HELHO, GEN14351, A28112_1, CET05A10_4 and P_W11485.

EXAMPLE 57: Isolation of cDNA Clones Encoding Human PRO273

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA36465. Based on the DNA36465 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO273.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CAGCGCCCTCCCCATGTCCCTG-3' (SEQ ID NO:371)

reverse PCR primer 5'-TCCCAACTGGTTTGGAGTTTTCCC-3' (SEQ ID NO:372)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA36465 sequence which had the following nucleotide sequence

hybridization probe

5'-CTCCGGTCAGCATGAGGCTCCTGGCGGCCGCTGCTCCTGCTGCTG-3' (SEQ ID NO:373)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO273 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO273 [herein designated as UNQ240 (DNA39523-1192)] (SEQ ID NO:369) and the derived protein sequence for PRO273.

The entire nucleotide sequence of UNQ240 (DNA39523-1192) is shown in Figure 148 (SEQ ID NO:369). Clone UNQ240 (DNA39523-1192) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 167-169 and ending at the stop codon at nucleotide positions 500-502 (Figure 148). The predicted polypeptide precursor is 111 amino acids long (Figure 149). Clone UNQ240 (DNA39523-1192) has been deposited with the ATCC. It is understood that the deposited clone contains the actual sequence and that the sequences provided herein are merely representative based on current sequencing techniques. Moreover, given the sequences provided herein and knowledge of the universal genetic code, the corresponding nucleotides for any given amino acid can be routinely identified and vice versa.

Analysis of the amino acid sequence of the full-length PRO273 polypeptide suggests that portions of it possess sequence identity with human macrophage inflammatory protein-2, cytokine-induced neutrophil chemoattractant 2, and neutrophil chemotactic factor 2-beta, thereby indicating that PRO273 is a novel chemokine.

As discussed further below, the cDNA was subcloned into a baculovirus vector and expressed in insect cells as a C-terminally tagged IgG fusion protein. N-terminal sequencing of the resultant protein identified the signal sequence cleavage site, yielding a mature polypeptide of 77 amino acids. The mature sequence, showing 31-40% identity to other human CXC chemokines, includes the four canonical cysteine residues but lacks the ELR motif. Northern analysis demonstrates expression at least in the small intestine, colon, spleen, lymph node and kidney. By in situ hybridization, also described in detail below, mRNA is localized to the lamina propria of intestinal villi and to renal tubules.

<u>EXAMPLE 58</u>: <u>Isolation of cDNA Clones Encoding Human PRO701</u>

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA39848. Based on the DNA39848 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO701.

A pair of PCR primers (forward and reverse) were synthesized:

<u>forward PCR primer</u> 5'-GGCAAGCTACGGAAACGTCATCGTG-3' (SEQ ID NO:376)

<u>reverse PCR primer</u> 5'-AACCCCCGAGCCAAAAGATGGTCAC-3' (SEQ ID NO:377)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA39848 sequence which had the following nucleotide sequence:

<u>hybridization probe</u>

5'-GTACCGGTGACCAGGCAGCAAAAGGCAACTATGGGCTCCTGGATCAG-3' (SEQ ID NO:378).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was

screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO701 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO701 [herein designated as UNQ365 (DNA44205-1285)] (SEQ ID NO:374) and the derived protein sequence for PRO701.

The entire nucleotide sequence of UNQ365 (DNA44205-1285) is shown in Figure 150 (SEQ ID NO:374). Clone UNQ365 (DNA44205-1285) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 50-52 and ending at the stop codon at nucleotide positions 2498-3000 (Figure 150). The predicted polypeptide precursor is 816 amino acids long (Figure 151). The full-length PRO701 protein shown in Figure 151 has an estimated molecular weight of about 91,794 daltons, a pI of about 5.88 and NX(S/T) being 4. Clone UNQ365 (DNA44205-1285) has been deposited with the ATCC on March 31, 1998. It is understood that the clone was the correct and actual sequence, wherein the sequences provided herein are representative based on sequencing techniques.

Still regarding the amino acid sequence shown in Figure 151, there is a potential signal peptide cleavage site at about amino acid 25. There are potential N-glycosylation sites at about amino acid positions 83, 511, 716 and 803. The carboxylesterases type-B signature 2 sequence is at about residues 125 to 135. Regions homologous with carboxylesterase type-B are also at about residues 54-74, 197-212 and 221-261. A potential transmembrane region corresponds approximately to amino acids 671 through about 700. The corresponding nucleic acids can be routinely determined from the sequences provided herein.

Analysis of the amino acid sequence of the full-length PRO701 polypeptide suggests that it possess significant homology to the neuroligins from rattus norvegicus indicating that PRO701 may be a novel human neuroligin.

EXAMPLE 59: Isolation of cDNA Clones Encoding Human PRO704

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA43033. Based on the DNA43033 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO704.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CCTTGGGTCGTGGCAGCAGTGG-3' (SEQ ID NO:381);

reverse PCR primer 5'-CACTCTCCAGGCTGCATGCTCAGG-3' (SEQ ID NO:382).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA43033 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-GTCAAACGTTCGAGTACTTGAAACGGGAGCACTCGCTGTCGAAGC-3' (SEQ ID NO:383).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO704 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO704 [herein designated as UNQ368 (DNA50911-1288)] (SEQ ID NO:379) and the derived protein sequence for PRO704.

The entire nucleotide sequence of UNQ368 (DNA50911-1288) is shown in Figure 152 (SEQ ID NO:379). Clone UNQ368 (DNA50911-1288) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 8-10 and ending at the stop codon at nucleotide positions 1052-1054 (Figure 152). The predicted polypeptide precursor is 348 amino acids long (Figure 153). The full-length PRO704 protein shown in Figure 153 has an estimated molecular weight of about 39,711 and a pI of about 8.7. Clone UNQ368 (DNA50911-1288) has been deposited with the ATCC on March 31, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO704 polypeptide suggests that portions of it possess significant homology to the vesicular integral membrane protein 36, thereby indicating that PRO704 may be a novel vesicular integral membrane protein.

Still analyzing the amino acid sequence of SEQ ID NO:380, the putative signal peptide is at about amino acids 1-39 of SEQ ID NO:380. The transmembrane domain is at amino acids 310-335 of SEQ ID NO:380. A potential N-glycosylation site is at about amino acids 180-183 of SEQ ID NO:380. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 60: Isolation of cDNA Clones Encoding Human PRO706

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA40669. Based on the DNA40669 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO706.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CCAAGCAGCTTAGAGCTCCAGACC-3' (SEQ ID NO:386)

reverse PCR primer 5'-TTCCCTATGCTCTGTATTGGCATGG-3' (SEQ ID NO:387)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA40669 sequence which had the following nucleotide sequence

hybridization probe

5'-GCCACTTCTGCCACAATGTCAGCTTTCCCTGTACCAGAAATGGCTGTGTT-3' (SEQ ID NO:388)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO706 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal brain tissue (LIB153).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO706 [herein designated as UNQ370 (DNA48329-1290)] (SEQ ID NO:384) and the derived protein sequence for PRO706. It is understood that the deposited clone contains the actual sequence, and that the sequences provided herein are representative based on current sequencing techniques.

The entire nucleotide sequence of UNQ370 (DNA48329-1290) is shown in Figure 154 (SEQ ID NO:384). Clone UNQ370 (DNA48329-1290) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 279-281 and ending at the stop codon at nucleotide positions 1719-1721 (Figure 154). The predicted polypeptide precursor is 480 amino acids long (Figure 155). The full-length PRO706 protein shown in Figure 155 has an estimated molecular weight of about 55,239 daltons and a pI of about 9.30. Clone UNQ370 (DNA48329-1290) has been deposited with the ATCC on April 21, 1998.

Still regarding the amino acid sequence shown in Figure 155, there is a potential signal peptide cleavage site at about amino acid 19. There are potential N-glycosylation sites at about amino acid positions 305 and 354. There is a potential tyrosine kinase phosphorylation site at about amino acid position 333. A region homologous with histidine acid phosphatase is at about residues 87-102. The corresponding nucleic acid regions can be routinely determined given the provided sequences, i.e., the codons can be determined from the specifically named amino acids given.

Analysis of the amino acid sequence of the full-length PRO706 polypeptide suggests that portions of it possess significant homology to the human prostatic acid phosphatase precursor thereby indicating that PRO706 may be a novel human prostatic acid phosphatase.

<u>EXAMPLE 61</u>: <u>Isolation of cDNA Clones Encoding Human PRO707</u>

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA42775. Based on DNA42775, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO707.

A pair of PCR primers (forward and reverse) were synthesized:

<u>forward PCR primer</u> 5'-TCCGTCTCTGTGAACCGCCCCAC-3' (SEQ ID NO:391);

<u>reverse PCR primer</u> 5'-CTCGGGCGCATTGTCGTTCTGGTC-3' (SEQ ID NO:392).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA42775 sequence which had the following nucleotide sequence:

<u>hybridization probe</u>

5'-CCGACTGTGAAAGAGAACGCCCCAGATCCACTTATTCCCC-3' (SEQ ID NO:393).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was

screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO707 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO707 [herein designated as UNQ371 (DNA48306-1291)] (SEQ ID NO:389) and the derived protein sequence for PRO707.

The entire nucleotide sequence of UNQ371 (DNA48306-1291) is shown in Figure 156 (SEQ ID NO:389). Clone UNQ371 (DNA48306-1291) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 371-373 and ending at the stop codon at nucleotide positions 3119-3121 of SEQ ID NO:389. The predicted polypeptide precursor is 916 amino acids long (Figure 157). The full-length PRO707 protein shown in Figure 157 has an estimated molecular weight of about 100,204 daltons and a pI of about 4.92. Clone UNQ371 (DNA48306-1291) has been deposited with ATCC on May 27, 1998. It is understood that the clone UNQ371 which is deposited is that which encodes PRO707, and that the sequences herein are merely representations based on known sequencing techniques which may be subject to minor errors.

Regarding analysis of the amino acid sequence, the signal sequence appears to be at about 1 through 30 of SEQ ID NO:390. Cadherins extracellular repeated domain signature sequence is at about amino acids 121-131, 230-240, 335-345, 440-450, and 550-560 of SEQ ID NO:390. Tyrosine kinase phosphorylation sites are at about amino acids 124-132 and 580-586 of SEQ ID NO:390. A potential transmembrane domain is at about amino acids 682-715 $\pm$ 5. The nucleic acid positions can be derived by referring to the corresponding codon for the named amino acid.

Analysis of the amino acid sequence of the full-length PRO707 polypeptide suggests that portions of it possess significant homology to the cadherin FIB3 protein, expressed in human fibroblasts, thereby indicating that PRO707 may be a novel cadherin.

EXAMPLE 62: Isolation of cDNA Clones Encoding Human PRO322

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA48336. Based on the DNA48336 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO322.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CAGCCTACAGAATAAAGATGGCCC-3' (SEQ ID NO:396)

reverse PCR primer 5'-GGTGCAATGATCTGCCAGGCTGAT-3' (SEQ ID NO:397)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA48336 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-AGAAATACCTGTGGTTCAGTCCATCCCAAACCCCTGCTACAACAGCAG-3' (SEQ ID NO:398).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO322 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO322 [herein designated as UNQ283 (DNA48336-1309)] (SEQ ID NO:394) and the derived protein sequence for PRO322. It is understood that UNQ283 (DNA48336-1309) in fact encodes PRO322, and that SEQ ID NO:394 is a representation of the sequence based on sequencing techniques known in the art.

The entire nucleotide sequence of UNQ283 (DNA48336-1309) is shown in Figure 158 (SEQ ID NO:394). Clone UNQ283 (DNA48336-1309) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 166-168 and ending at the stop codon at nucleotide positions 946-948 (Figure 158). The predicted polypeptide precursor is 260 amino acids long (Figure 159). The full-length PRO322 protein shown in Figure 159 has an estimated molecular weight of about 28,028 daltons and a pI of about 7.87. Clone UNQ283 (DNA48336-1309) has been deposited with ATCC and is assigned ATCC deposit no. 209669.

Regarding the amino acid sequence of Figure 159, a potential N-glycosylation site is at amino acid 110 of SEQ ID NO:395. The serine proteases, trypsin family and histidine active site is identified at amino acids 69 through 74 of SEQ ID NO:395 and the consensus sequence is identified at amino acids 207 through 217 of SEQ ID NO:395. The kringle domain proteins motif is identified at amino acids 205 through 217 of SEQ ID NO:395. The putative signal peptide is encoded at about amino acids 1-23.

Analysis of the amino acid sequence of the full-length PRO322 polypeptide suggests that portions of it possess significant homology to neuropsin and other serine proteases, thereby indicating that PRO322 is a novel serine protease related to neuropsin.

EXAMPLE 63: Isolation of cDNA Clones Encoding Human PRO526

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA39626. Based on the DNA39626 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO526.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-TGGCTGCCCTGCAGTACCTCTACC-3' (SEQ ID NO:401);

reverse PCR primer 5'-CCCTGCAGGTCATTGGCAGCTAGG-3' (SEQ ID NO:402).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA39626 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-AGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCACAC-3' (SEQ ID NO:403).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO526 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal liver tissue (LIB228).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO526 [herein designated as UNQ330 (DNA44184-1319)] (SEQ ID NO:399) and the derived protein sequence for PRO526.

The entire nucleotide sequence of UNQ330 (DNA44184-1319) is shown in Figure 160 (SEQ ID NO:399). Clone UNQ330 (DNA44184-1319) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 514-516 and ending at the stop codon at nucleotide positions 1933-1935 (Figure 160). The predicted polypeptide precursor is 473 amino acids long (Figure 161). The full-length PRO526 protein shown in Figure 161 has an estimated molecular weight of about 50,708 daltons and a pI of about 9.28. Clone UNQ330 (DNA44184-1319) has been deposited with the ATCC on March 26, 1998. It is understood that the clone contains the actual sequence, whereas the sequences presented herein are representative based on current sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO526 polypeptide suggests that portions of it possess significant homology to the leucine repeat rich proteins including ALS, SLIT, carboxypeptidase and platelet glycoprotein V thereby indicating that PRO526 is a novel protein which is involved in protein-protein interactions.

Still analyzing SEQ ID NO:400, the signal peptide sequence is at about amino acids 1-26. A leucine zipper pattern is at about amino acids 135-156. A glycosaminoglycan attachment is at about amino acids 436-439. N-glycosylation sites are at about amino acids 82-85, 179-182, 237-240 and 423-426. A von Willebrand factor (VWF) type C domain(s) is found at about amino acids 411-425. The skilled artisan can understand which nucleotides correspond to these amino acids based on the sequences provided herein.

EXAMPLE 64: Isolation of cDNA Clones Encoding Human PRO531

An ECD database was searched and an expressed sequence tag (EST) from LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA was identified which showed homology to protocadherin 3. Based on this sequence, a search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequence. Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Washington; http://bozeman.mbt.washington.edu/phrap.docs/phrap.html).

A consensus DNA sequence was assembled relative to other EST sequences using phrap. Based on the

consensus sequence obtained, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO531.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CTGAGAACGCGCCTGAAACTGTG-3' (SEQ ID NO:406);

reverse PCR primer 5'-AGCGTTGTCATTGACATCGGCG-3' (SEQ ID NO:407).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA sequence which had the following nucleotide sequence:

hybridization probe

5'-TTAGTTGCTCCATTCAGGAGGATCTACCCTTCCTCCTGAAATCCGCGGAA-3' (SEQ ID NO:408).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO531 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal brain tissue (LIB153). The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO531 [herein designated as UNQ332 (DNA48314-1320)] (SEQ ID NO:404) and the derived protein sequence for PRO531.

The entire representative nucleotide sequence of UNQ332 (DNA48314-1320) is shown in Figure 162 (SEQ ID NO:404). It is understood that the actual sequence is that within the clone deposited with the ATCC as DNA48314-1320. Clone UNQ332 (DNA48314-1320) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 171-173 and ending at the stop codon at nucleotide positions 2565-2567 (Figure 162). The predicted polypeptide precursor is 789 amino acids long (Figure 163). The full-length PRO531 protein shown in Figure 163 has an estimated molecular weight of about 87,552 daltons and a pI of about 4.84. Clone UNQ332 (DNA48314-1320) has been deposited with the ATCC on March 26, 1998.

Analysis of the amino acid sequence of the full-length PRO531 polypeptide suggests that portions of it possess significant homology to protocadherin 3. Moreover, PRO531 is found in the brain, like other protocadherins; thereby indicating that PRO531 is a novel member of the cadherin superfamily.

Still analyzing the amino acid sequence of SEQ ID NO:405, the cadherin extracellular repeated domain signature is found at about amino acids 122-132, 231-241, 336-346, 439-449 and 549-559 of SEQ ID NO:405. An ATP/GTP-binding site motif A (P-loop) is found at about amino acids 285-292 of SEQ ID NO:405. N-glycosylation sites are found at least at about amino acids 567-570, 786-790, 418-421 and 336-339 of SEQ ID

NO:405. The signal peptide is at about amino acids 1-26, and the transmembrane domain is at about amino acids 685-712 of SEQ ID NO:405.

EXAMPLE 65: Isolation of cDNA Clones Encoding Human PRO534

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA43038. Based on the 43048 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO534.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CACAGAGCCAGAAGTGGCGGAATC-3' (SEQ ID NO:411);

reverse PCR primer 5'-CCACATGTTCCTGCTCTTGTCCTGG-3' (SEQ ID NO:412).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA43038 sequence which had the following nucleotide sequence:

hybridization probe

5'-CGGTAGTGACTGTACTCTAGTCCTGTTTTACACCCCGTGGTGCCG-3' (SEQ ID NO:413).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO534 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal lung tissue (LIB26).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO534 [herein designated as UNQ335 (DNA48333-1321)] (SEQ ID NO:409) and the derived protein sequence for PRO534.

The entire nucleotide sequence of UNQ335 (DNA48333-1321) is shown in Figure 164 (SEQ ID NO:409). Clone UNQ335 (DNA48333-1321) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 87-89 and ending at the stop codon at nucleotide positions 1167-1169 (Figure 164). The predicted polypeptide precursor is 360 amino acids long (Figure 165). The full-length PRO534 protein shown in Figure 165 has an estimated molecular weight of about 39,885 daltons and a pI of about 4.79. Clone UNQ335 (DNA48333-1321) has been deposited with ATCC on March 26, 1998. It is understood that the deposited clone contains the actual sequence, and that the sequences provided herein are representative based on current sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO534 polypeptide suggests that portions of it possess significant sequence identity with the protein disulfide isomerase, thereby indicating that PRO534 may be a novel disulfide isomerase.

Still analyzing the amino acid sequence of PRO534, the signal peptides is at about amino acids 1-25 of SEQ ID NO:410. The transmembrane domain is at about amino acids 321-340 of SEQ ID NO:410. The disulfide isomerase corresponding region is at amino acids 212-302 of SEQ ID NO:410. The thioredoxin domain is at amino acids 211-227 of SEQ ID NO:410. N-glycosylation sites are at: 165-168, 181-184, 187-190, 194-

197, 206-209, 278-281, and 293-296 of SEQ ID NO:410. The corresponding nucleotides can routinely be determined from the sequences provided herein. PRO534 has a transmembrane domain rather than an ER retention peptide like other protein disulfide isomerases. Additionally, PRO534 may have an intron at the 5 prime end.

EXAMPLE 66: Isolation of cDNA Clones Encoding Human PRO697

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA43052. Based on this consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO697.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CCTGGCTCGCTGCTGCTGCTC-3' (SEQ ID NO:416);

reverse PCR primer 5'-CCTCACAGGTGCACTGCAAGCTGTC-3' (SEQ ID NO:417).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA43052 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-CTCTTCCTCTTTGGCCAGCCCGACTTCTCCTACAAGCGCAGAATTGC-3' (SEQ ID NO:418).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO697 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO697 [herein designated as UNQ361 (DNA50920-1325)] (SEQ ID NO:414) and the derived protein sequence for PRO697.

The entire nucleotide sequence of UNQ361 (DNA50920-1325) is shown in Figure 166 (SEQ ID NO:414). Clone UNQ361 (DNA50920-1325) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 44-46 and ending at the stop codon at nucleotide positions 929-931 (Figure 166). The predicted polypeptide precursor is 295 amino acids long (Figure 167). The full-length PRO697 protein shown in Figure 167 has an estimated molecular weight of about 33,518 daltons and a pI of about 7.74. Clone UNQ361 (DNA50920-1325) was deposited with the ATCC on March 26, 1998. It is understood that the deposited clone contains the actual sequence, and that the sequences provided herein are representative based on current sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO697 polypeptide suggests that portions of it possess significant sequence identity with sFRPs, thereby indicating that PRO697 may be a novel sFRP family member.

Still analyzing the amino acid sequence of PRO697, the signal peptides is at about amino acids 1-20 of SEQ ID NO:415. The cystein rich domain, having identity with the frizzled N-terminus, is at about amino acids

6-153 of SEQ ID NO:415. The corresponding nucleotides can routinely be determined from the sequences provided herein.

EXAMPLE 67: Isolation of cDNA Clones Encoding Human PRO717

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA42829. Based on the DNA42829 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO717.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-AGCTTCTCAGCCCTCCTGGAGCAG-3' (SEQ ID NO:421);

reverse PCR primer 5'-CGGGTCAATAAACCTGGACGCTTGG-3' (SEQ ID NO:422).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA42829 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-TATGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTG-3' (SEQ ID NO:423).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO717 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal liver tissue (LIB229).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO717 [herein designated as UNQ385 (DNA50988-1326)] (SEQ ID NO:419) and the derived protein sequence for PRO717.

The entire nucleotide sequence of UNQ385 (DNA50988-1326) is shown in Figure 168 (SEQ ID NO:419). Clone UNQ385 (DNA50988-1326) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 17-19 and ending at the stop codon at nucleotide positions 1697-1699 (Figure 168). The predicted polypeptide precursor is 560 amino acids long (Figure 169). The full-length PRO717 protein shown in Figure 169 has an estimated molecular weight of about 58,427 daltons and a pI of about 6.86. Clone UNQ385 (DNA50988-1326) has been deposited with the ATCC on April 28, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO717 polypeptide suggests that PRO717 may be a novel 12 transmembrane receptor. The reverse complement strand of DNA50988 has a stretch that matches identically with human regulatory myosin light strand.

Still analyzing the amino acid sequence of SEQ ID NO:420, transmembrane domains are at about amino acids 30-50, 61-79, 98-112, 126-146, 169-182, 201-215, 248-268, 280-300, 318-337, 341-357, 375-387, and 420-441 of SEQ ID NO:420. N-glycosylation sites are at about amino acids 40-43 and 43-46 of SEQ ID

NO:420. A glycosaminoglycan attachment site is at about amino acids 468-471 of SEQ ID NO:420. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 68: Isolation of cDNA Clones Encoding Human PRO731

A database was used to search expressed sequence tag (EST) databases. The EST database used herein was the proprietary EST DNA database LIFESEQ™, of Incyte Pharmaceuticals, Palo Alto, CA. Incyte clone 2581326 was herein identified and termed DNA42801. Based on the DNA42801 sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO731.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GTAAGCACATGCCTCCAGAGGTGC-3' (SEQ ID NO:426);

reverse PCR primer 5'-GTGACGTGGATGCTTGGGATGTTG-3' (SEQ ID NO:427).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA42801 sequence which had the following nucleotide sequence:

hybridization probe

5'-TGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTCATTCTGCGTCGA-3' (SEQ ID NO:428).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO731 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human bone marrow tissue (LIB255). The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO731 [herein designated as UNQ395 (DNA48331-1329)] (SEQ ID NO:424) and the derived protein sequence for PRO731.

The entire nucleotide sequence of UNQ395 (DNA48331-1329) is shown in Figures 170A-B (SEQ ID NO:424). Clone UNQ395 (DNA48331-1329) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 329-331 and ending at the stop codon at nucleotide positions 3881-3883 (Figures 170A-B). The predicted polypeptide precursor is 1184 amino acids long (Figure 171). The full-length PRO731 protein shown in Figure 171 has an estimated molecular weight of about 129,022 daltons and a pI of about 5.2. Clone UNQ395 (DNA48331-1329) was deposited with the ATCC on March 31, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO731 polypeptide suggests that portions of it possess significant identity and similarity to members of the protocadherin family, thereby indicating that PRO731 may be a novel protocadherin.

Still analyzing the amino acid sequence of SEQ ID NO:425, the putative signal peptide is at about amino acids 1-13 of SEQ ID NO:425. The transmembrane domain is at amino acids 719-739 of SEQ ID NO:425. The N-glycosylation of SEQ ID NO:425 are as follows: 415-418, 582-586, 659-662, 662-665, and 857-860. The cadherin extracellular repeated domain signatures are at about amino acids (of SEQ ID NO:425): 123-133, 232-242, 340-350, 448-458, and 553-563. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 69: Isolation of cDNA Clones Encoding Human PRO218

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA17411. Two proprietary Genentech EST sequences were employed in the consensus assembly and are shown in Figure 174 and 175. Based on the DNA17411 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO218.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-AAGTGGAGCCGGAGCCTTCC-3' (SEQ ID NO:433);

reverse PCR primer 5'-TCGTTGTTTATGCAGTAGTCGG-3' (SEQ ID NO:434).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA17411 sequence which had the following nucleotide sequence:

hybridization probe

5'-ATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGG-3' (SEQ ID NO:435).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO218 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB28).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO218 [herein designated as UNQ192 (DNA30867-1335)] (SEQ ID NO:429) and the derived protein sequence for PRO218.

The entire nucleotide sequence of UNQ192 (DNA30867-1335) is shown in Figure 172 (SEQ ID NO:429). Clone UNQ192 (DNA30867-1335) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 150-152 and ending at the stop codon at nucleotide positions 1515-1517 (Figure 172). The predicted polypeptide precursor is 455 amino acids long (Figure 173). The full-length PRO218 protein shown in Figure 173 has an estimated molecular weight of about 52,917 daltons and a pI of about 9.5. Clone UNQ192 (DNA30867-1335) has been deposited with the ATCC on April 28, 1998. Regarding

the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO218 polypeptide suggests that PRO218 may be a novel transmembrane protein.

Still analyzing the amino acid sequence of SEQ ID NO:430, the putative signal peptide is at about amino acids 1 through 23 of SEQ ID NO:430. Transmembrane domains are potentially at about amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398, and 425-444 of SEQ ID NO:430. N-glycosylation sites are at about amino acids 67, 180, and 243 of SEQ ID NO:430. Eukaryotic cobalamin-binding protein is at about amino acids 151-160 of SEQ ID NO:430. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 70: Isolation of cDNA Clones Encoding Human PRO768

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA43448. Based on the DNA43448 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO768.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GGCTGACACCGCAGTGCTCTTCAG-3' (SEQ ID NO:438);

reverse PCR primer 5'-GCTGCTGGGGACTGCAATGTAGCTG-3' (SEQ ID NO:439).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA43448 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-CATCCTCCATGTCTCCCATGAGGTCTCTATTGCTCCACGAAGCATC-3' (SEQ ID NO:440).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO768 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human bone marrow tissue (LIB255).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO768 [herein designated as UNQ406 (DNA55737-1345)] (SEQ ID NO:436) and the derived protein sequence for PRO768.

The entire nucleotide sequence of UNQ406 (DNA55737-1345) is shown in Figures 176A-B (SEQ ID NO:436). Clone UNQ406 (DNA55737-1345) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 20-22 and ending at the stop codon at nucleotide positions 3443-3445 (Figures 176A-B). The predicted polypeptide precursor is 1141 amino acids long (Figure 177). The full-length PRO768 protein shown in Figure 177 has an estimated molecular weight of about 124,671 daltons and a pI of about 5.82. Clone UNQ406 (DNA55737-1345) has been deposited with the ATCC on April 6, 1998. Regarding

the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO768 polypeptide suggests that portions of it possess significant sequence identity and similarity with integrin 7.

Still analyzing the amino acid sequence of SEQ ID NO:437, the putative signal peptide is at about amino acids 1-33 of SEQ ID NO:437. The transmembrane domain is at amino acids 1039-1064 of SEQ ID NO:437. N-glycosylation sites are at amino acids: 86-89, 746-749, 949-952, 985-988 and 1005-1008 of SEQ ID NO:437. Integrin alpha chain protein domains are identified at about amino acids: 1064-1071, 384-409, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047 of SEQ ID NO:437. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 71: Isolation of cDNA Clones Encoding Human PRO771

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA43330. Based on the DNA43330 sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO771.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CAGCAATATTCAGAAGCGGCAAGGG-3' (SEQ ID NO:443);

reverse PCR primer 5'-CATCATGGTCATCACCACCATCATCATC-3' (SEQ ID NO:444).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA43330 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-GGTTACTACAAGCCAACACAATGTCATGGCAGTGTTGGACAGTGCTGG-3' (SEQ ID NO:445).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO771 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB28).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO771 [herein designated as UNQ409 (DNA49829-1346)] (SEQ ID NO:441) and the derived protein sequence for PRO771.

The entire nucleotide sequence of UNQ409 (DNA49829-1346) is shown in Figure 178 (SEQ ID NO:441). Clone UNQ409 (DNA49829-1346) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 134-136 and ending at the stop codon at nucleotide positions 1442-1444 (Figure 178). The predicted polypeptide precursor is 436 amino acids long (Figure 179). The full-length PRO771 protein shown in Figure 179 has an estimated molecular weight of about 49,429 daltons and a pI of about 4.8. Clone UNQ409 (DNA49829-1346) has been deposited with the ATCC on April 7, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided

herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO771 polypeptide suggests that portions of it possess significant homology to the testican protein, thereby indicating that PRO771 may be a novel testican homologue.

Still analyzing the amino acid sequence of SEQ ID NO:442, the putative signal peptide, leucine zipper pattern, N-myristoylation sites, and thyroglobulin type-1 repeats are also shown in Figure 179. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 72: Isolation of cDNA Clones Encoding Human PRO733

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA45600. Based on the DNA45600 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO733.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CCCAGCAGGGATGGGCGACAAGA-3' (SEQ ID NO:448);

reverse PCR primer 5'-GTCTTCCAGTTTCATATCCAATA-3' (SEQ ID NO:449).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA45600 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-CCAGAAGGAGCACGGGGAAGGGCAGCCAGATCTTGTCGCCCAT-3' (SEQ ID NO:450).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO733 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human bone marrow tissue (LIB255).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO733 [herein designated as UNQ411 (DNA52196-1348)] (SEQ ID NO:446) and the derived protein sequence for PRO733.

The entire nucleotide sequence of UNQ411 (DNA52196-1348) is shown in Figures 180A-B (SEQ ID NO:446). Clone UNQ411 (DNA52196-1348) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 106-108 and ending at the stop codon at nucleotide positions 793-795 (Figures 180A-B). The predicted polypeptide precursor is 229 amino acids long (Figure 181). The full-length PRO733 protein shown in Figure 181 has an estimated molecular weight of about 26,017 daltons and a pI of about 4.73. Clone UNQ411 (DNA52196-1348) has been deposited with the ATCC on April 7, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO733 polypeptide suggests that portions of it possess significant sequence identity and similarity to the T1/ST2 receptor binding protein precursor and therefore may have a similar function in cell signaling. If it is a cytokine, it may be useful in the treatment of inflammation and cancer.

Still analyzing the amino acid sequence of SEQ ID NO:447, the putative signal peptide, transmembrane domain, N-myristoylation site, and tyrosine kinase site are also shown in Figure 181. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 73: Isolation of cDNA Clones Encoding Human PRO162

An expressed sequence tag (EST) DNA database (Merck/Washington University) was searched and an EST AA397543 was identified which showed homology to human pancreatitis-associated protein. The EST AA397543 cole was purchased and its insert obtained and sequenced and the sequence obtained is shown in Figure 182 (SEQ ID NO:451).

The entire nucleotide sequence of PRO162 is shown in Figure 182 (SEQ ID NO:451). DNA sequencing of the clone gave the full-length DNA sequence for PRO162 [herein designated as UNQ429 (DNA56965-1356)] (SEQ ID NO:451) and the derived protein sequence for PRO162. Clone UNQ429 (DNA56965-1356) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 86-88 and ending at the stop codon at nucleotide positions 611-613 (Figure 182). The predicted polypeptide precursor is 175 amino acids long (Figure 183). The full-length PRO162 protein shown in Figure 183 has an estimated molecular weight of about 19,330 daltons and a pI of about 7.25. Clone UNQ429 (DNA56965-1356) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO162 polypeptide suggests that portions of it possess significant homology to the human pancreatitis-associated protein, thereby indicating that PRO162 may be a novel pancreatitis-associated protein.

Still analyzing the amino acid sequence of SEQ ID NO:452, the putative signal peptide is at about amino acids 1-26 of SEQ ID NO:452. A C-type lectin domain signature is at about amino acids 146-171 of SEQ ID NO:452. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 74: Isolation of cDNA Clones Encoding Human PRO788

A consensus DNA sequence (designated herein as DNA49308) was assembled relative to other EST sequences using phrap as described in Example 1 above. Based upon an observed homology between the DNA49308 consensus sequence and the Incyte EST clo0ne no. 2777282, the Incyte EST clone no. 2777282 was purchased and its insert obtained and sequenced, which gave the full-length DNA sequence for PRO788 [herein designated as UNQ430 (DNA56405-1357)] (SEQ ID NO:453) and the derived protein sequence for PRO788.

Clone UNQ430 (DNA56405-1357) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 84-86 and ending at the stop codon at nucleotide positions 459-461 (Figure

184). The predicted polypeptide precursor is 125 amino acids long (Figure 185). The full-length PRO788 protein shown in Figure 185 has an estimated molecular weight of about 13,115 daltons and a pI of about 5.90. Clone UNQ430 (DNA56405-1357) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Still analyzing Figure 185, a signal peptide is shown at about amino acids 1-17 of SEQ ID NO:454. An N-glycosylation site is at about amino acids 46-49 of SEQ ID NO:454.

EXAMPLE 75: Isolation of cDNA Clones Encoding Human PRO1008

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated as DNA49804. An EST proprietary to Genentech was employed in the consensus assembly and is herein designated as DNA16508 (Figure 188; SEQ ID NO:457). Based upon an observed homology between the DNA49804 sequence and Merck EST clone no. AA143670, the Merck EST clone no. AA143670 was purchased and its insert obtained and sequenced. That sequence is shown herein in Figure 186 (SEQ ID NO:455).

Sequencing gave the full length sequence for PRO1008 [herein designated as UNQ492 (DNA57530-1375)] (SEQ ID NO:455) and the derived protein sequence for PRO1008 were identified.

The entire nucleotide sequence of UNQ492 (DNA57530-1375) is shown in Figure 186 (SEQ ID NO:455). Clone UNQ492 (DNA57530-1375) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 138-140 and ending at the stop codon at nucleotide positions 936-938 (Figure 186). The predicted polypeptide precursor is 266 amino acids long (Figure 187). The full-length PRO1008 protein shown in Figure 187 has an estimated molecular weight of about 28,672 daltons and a pI of about 8.85. Clone UNQ492 (DNA57530-1375) has been deposited with the ATCC on May 20, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO1008 polypeptide suggests that portions of it possess significant sequence identity and/or similarity with mdkk-1, thereby indicating that PRO1008 may be a novel member of this family and have head inducing activity.

Still analyzing the amino acid sequence of SEQ ID NO:456, the putative signal peptide is at about amino acids 1-23 of SEQ ID NO:456. The N-glycosylation site is at about amino acids 256-259 of SEQ ID NO:456, and the fungal zn-(2)-cys(6) binuclear cluster domain is at about amino acids 110-126 of SEQ ID NO:456. The corresponding nucleotides can of all the amino acids can be routinely determined given the sequences provided herein.

EXAMPLE 76: Isolation of cDNA Clones Encoding Human PRO1012

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above, wherein the consensus sequence is herein designated DNA49313. Based on the DNA49313

consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO1012.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-ACTCCCCAGGCTGTTCACACTGCC-3' (SEQ ID NO:460);

reverse PCR primer 5'-GATCAGCCAGCCAATACCAGCAGC-3' (SEQ ID NO:461).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA49313 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-GTGGTGATGATAGAATGCTTTGCCGAATGAAAGGAGTCAACAGCTATCCC-3' (SEQ ID NO:462).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO1012 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO1012 [herein designated as UNQ495 (DNA56439-1376)] (SEQ ID NO:458) and the derived protein sequence for PRO1012.

The entire nucleotide sequence of UNQ495 (DNA56439-1376) is shown in Figures 189A-B (SEQ ID NO:458). Clone UNQ495 (DNA56439-1376) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 404-406 and ending at the stop codon at nucleotide positions 2645-2647 (Figures 189A-B). The predicted polypeptide precursor is 747 amino acids long (Figure 190). The full-length PRO1012 protein shown in Figure 190 has an estimated molecular weight of about 86,127 daltons and a pI of about 7.46. Clone UNQ495 (DNA56439-1376) has been deposited with ATCC on May 14, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO1012 polypeptide suggests that portions of it possess sequence identity with disulfide isomerase thereby indicating that PRO1012 may be a novel disulfide isomerase related protein.

Still analyzing the amino acid sequence of SEQ ID NO:459, the cytochrome C family heme-binding site signature is at about amino acids 158-163 of SEQ ID NO:459. The Nt-DNAJ domain signature is at about amino acids 77-96 of SEQ ID NO:459. An N-glycosylation site is at about amino acids 484-487 of SEQ ID NO:459. The ER targeting sequence is at about amino acids 744-747 of SEQ ID NO:459. It is understood that the polypeptide and nucleic acids disclosed can be routinely formed with or without, these portions as desired, in alternative embodiments. For example, it may be desirable to produce PRO1012 without the ER targeting sequence. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 77: Isolation of cDNA Clones Encoding Human PRO1014

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 abobe, wherein the consensus sequence obtained is herein designated DNA49811. Based upon an observed homology between the DNA49811 sequence and Incyte EST clone no. 2612207, Incyte EST clone no. 2612207 was purchased and its insert was obtained and sequenced, wherein the sequence obtained is shown in Figure 191 (SEQ OD NO:463).

DNA sequencing gave the full-length DNA sequence for PRO1014 [herein designated as UNQ497 (DNA56409-1377)] (SEQ ID NO:463) and the derived protein sequence for PRO1014.

The entire nucleotide sequence of UNQ497 (DNA56409-1377) is shown in Figure 191 (SEQ ID NO:463). Clone UNQ497 (DNA56409-1377) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 66-68 and ending at the stop codon at nucleotide positions 966-968 (Figure 191). The predicted polypeptide precursor is 300 amino acids long (Figure 192). The full-length PRO1014 protein shown in Figure 192 has an estimated molecular weight of about 33,655 daltons and a pI of about 9.31. Clone UNQ497 (DNA56409-1377) has been deposited with the ATCC on May 20, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO1014 polypeptide suggests that portions of it possess sequence identity with reductase, thereby indicating that PRO1014 may be a novel member of the reductase family.

Still analyzing the amino acid sequence of SEQ ID NO:464, the putative signal peptide is at about amino acids 1-19 of SEQ ID NO:464. The cAMP and cGMP dependent protein kinase phosphorylation sites are at about amino acids 30-33 and 58-61 of SEQ ID NO:464. Short chain alcohol dehydrogenase family proteins are at about amino acids 165-202, 37-49, 112-122 and 210-219 of SEQ ID NO:464. The corresponding nucleotides of these domains and any other amino acids provided herein can be routinely determined given the sequences provided herein.

EXAMPLE 78: Isolation of cDNA Clones Encoding Human PRO1017

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above, wherein that consensus DNA sequence is herein designated DNA53235. Based upon an observed homology between the DNA53235 consensus sequence and the Merck EST clone no. AA243086, the Merck EST clone no. AA243086 was purchased and its insert obtained and sequenced, wherein the sequence obtained is shown in Figure 193 (SEQ ID NO:465). DNA sequencing gave the full-length DNA sequence for PRO1017 [herein designated as UNQ500 (DNA56112-1379)] (SEQ ID NO:465) and the derived protein sequence for PRO1017.

The entire nucleotide sequence of UNQ500 (DNA56112-1379) is shown in Figure 193 (SEQ ID NO:465). Clone UNQ500 (DNA56112-1379) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 128-130 and ending at the stop codon at nucleotide positions 1370-1372

(Figure 193). The predicted polypeptide precursor is 414 amino acids long (Figure 194). The full-length PRO1017 protein shown in Figure 194 has an estimated molecular weight of about 48,414 daltons and a pI of about 9.54. Clone UNQ500 (DNA56112-1379) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO1017 polypeptide suggests that portions of it possess sequence identity with HNK-1 sulfotransferase, thereby indicating that PRO1017 may be a novel sulfotransferase.

Still analyzing the amino acid sequence of SEQ ID NO:466, the putative signal peptide is at about amino acids 1-31 of SEQ ID NO:466. N-glycosylation sites are at about amino acids 134-137, 209-212, 280-283 and 370-273 of SEQ ID NO:466. The TNFR/NGFR family cystein-rich region protein is at about amino acids 329-332 of SEQ ID NO:466. The corresponding nucleotides can be routinely determined given the sequences provided herein. The protein can be secreted.

EXAMPLE 79: Isolation of cDNA Clones Encoding Human PRO474

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA49818. Based upon an observed homology between the DNA49818 consensus sequence and the Merck EST clone no. H77889, the Merck EST clone no. H77889 was purchased and its insert obtained and sequenced, wherein the sequence obtained is herein shown in Figure 195 (SEQ ID NO:467). DNA sequencing gave the full-length DNA sequence for PRO474 [herein designated as UNQ502 (DNA56045-1380)] (SEQ ID NO:467) and the derived protein sequence for PRO474.

The entire nucleotide sequence of UNQ502 (DNA56045-1380) is shown in Figure 195 (SEQ ID NO:467). Clone UNQ502 (DNA56045-1380) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 106-108 and ending at the stop codon at nucleotide positions 916-918 (Figure 195). The predicted polypeptide precursor is 270 amino acids long (Figure 196). The full-length PRO474 protein shown in Figure 196 has an estimated molecular weight of about 28,317 daltons and a pI of about 6.0. Clone UNQ502 (DNA56045-1380) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Still analyzing the amino acid sequence of SEQ ID NO:468, an N-glycosylation site is at about amino acids 138-141 of SEQ ID NO:468. Short-chain alcohol dehydrogenase family proteins are at about amino acids 10-22, 81-91, 134-171 and 176-185 of SEQ ID NO:468. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 80: Isolation of cDNA Clones Encoding Human PRO1031

An initial consensus DNA sequence was assembled relative to other EST sequences using phrap as

described in Example 1 above, wherein the consensus sequence obtained is herein designated as DNA47332. Based upon an observed homology between the DNA47332 sequence and the Merck EST clone no. W74558, Merck EST clone no. W74558 was purchased and its insert obtained and sequenced, wherein the sequence obtained is shown in Figure 197 (SEQ ID NO:469). DNA sequencing gave the full-length DNA sequence for PRO1031 [herein designated as UNQ516 (DNA59294-1381)] (SEQ ID NO:469) and the derived protein sequence for PRO1031.

The entire nucleotide sequence of UNQ516 (DNA59294-1381) is shown in Figure 197 (SEQ ID NO:469). Clone UNQ516 (DNA59294-1381) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 42-44 and ending at the stop codon at nucleotide positions 582-584 (Figure 197). The predicted polypeptide precursor is 180 amino acids long (Figure 198). The full-length PRO1031 protein shown in Figure 198 has an estimated molecular weight of about 20,437 daltons and a pI of about 9.58. Clone UNQ516 (DNA59294-1381) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO1031 polypeptide suggests that it is a novel cytokine.

Still analyzing the amino acid sequence of SEQ ID NO:470, the putative signal peptide is at about amino acids 1-20 of SEQ ID NO:470. An N-glycosylation site is at about amino acids 75-78 of SEQ ID NO:470. A region having sequence identity with IL-17 is at about amino acids 96-180. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 81: Isolation of cDNA Clones Encoding Human PRO938

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above, wherein that consensus sequence is herein designated DNA49798. Based on the DNA49798 DNA consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO938.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GTCCAGCCCATGACCGCCTCCAAC-3' (SEQ ID NO:473)

reverse PCR primer 5'-CTCTCCTCATCCACACCAGCAGCC-3' (SEQ ID NO:474)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA49798 sequence which had the following nucleotide sequence:

hybridization probe

5'-GTGGATGCTGAAATTTTACGCCCCATGGTGTCCATCCTGCCAGC-3' (SEQ ID NO:475)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO938 gene using the probe oligonucleotide and one of the PCR primers. RNA

for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO938 [herein designated as UNQ475 (DNA56433-1406)] (SEQ ID NO:471) and the derived protein sequence for PRO938.

The entire nucleotide sequence of UNQ475 (DNA56433-1406) is shown in Figure 199 (SEQ ID NO:471). Clone UNQ475 (DNA56433-1406) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 134-136 and ending at the stop codon at nucleotide positions 1181-1183 (Figure 199). The predicted polypeptide precursor is 349 amino acids long (Figure 200). The full-length PRO938 protein shown in Figure 200 has an estimated molecular weight of about 38,952 daltons and a pI of about 4.34. Analysis of the full-length PRO938 sequence shown in Figure 200 (SEQ ID NO:472) evidences the presence of the following features: a signal peptide from amino 1 to about amino acid 22, a transmembrane domain from about amino acid 191 to about amino acid 211, a potential N-glycosylation site from about amino acid 46 to about amino acid 49, a region homologous to disulfide isomerase from about amino acid 56 to about amino acid 72, and a region having sequence identity with flavodoxin proteins from about amino acid 173 to about amino acid 187.

Clone UNQ475 (DNA56433-1406) has been deposited with ATCC on May 12, 1998, and is assigned ATCC Accession No. 209857.

Analysis of the amino acid sequence of the full-length PRO938 polypeptide suggests that it possesses significant sequence similarity to protein disulfide isomerase, thereby indicating that PRO938 may be a novel protein disulfide isomerase. An analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO938 amino acid sequence and the following Dayhoff sequences, P_W03626, P_W03627, P_R70491, GARP_PLAFF, XLU85970_1, ACADISPROA_1, IE68_HSVSA, KSU52064_1, U93872_83, P_R97866.

EXAMPLE 82: Isolation of cDNA Clones Encoding Human PRO1082

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above, wheein the consensus sequence is herein designated DNA38097. Based on this consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO1082.

A set of PCR primers (two forward and one reverse) were synthesized:

forward primer 1 5'-GTCCACAGACAGTCATCTCAGGAGCAG-3' (SEQ ID NO:478);

forward primer 2 5'-ACAAGTGTCTTCCCAACCTG-3' (SEQ ID NO:479);

reverse primer 1 5'-ATCCTCCCAGAGCCATGGTACCTC-3' (SEQ ID NO:480).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA38097 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-CCAAGGATAGCTGTTGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCT-3' (SEQ ID NO:481).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primers identified above. A positive library was then used to isolate clones encoding the PRO1082 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO1082 [herein designated as UNQ539 (DNA53912-1457)] (SEQ ID NO:476) and the derived protein sequence for PRO1082.

The entire nucleotide sequence of UNQ539 (DNA53912-1457) is shown in Figure 201 (SEQ ID NO:476). Clone UNQ539 (DNA53912-1457) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 160-162 and ending at the stop codon at nucleotide positions 763-765 (Figure 201). The predicted polypeptide precursor is 201 amino acids long (Figure 202). The full-length PRO1082 protein shown in Figure 202 has an estimated molecular weight of about 22,563 daltons and a pI of about 4.87. Clone UNQ539 (DNA53912-1457) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Still analyzing the amino acid sequence of SEQ ID NO:477, the transmembrane domain is at about amino acids 45-65 of SEQ ID NO:477. A cAMP- and cGMP-dependent protein kinase phosphorylation site is at about amino acids 197-200 of SEQ ID NO:477. N-myristoylation sites are at about amino acids 35-40 and 151-156 of SEQ ID NO:477. The regions which share sequence identity with the LDL receptor are at about amino acids 34-67 and 70-200 of SEQ ID NO:477. The corresponding nucleotides of these amino acid regions and others can be routinely determined given the sequences provided herein.

<u>EXAMPLE 83</u>: <u>Isolation of cDNA Clones Encoding Human PRO1083</u>

A cDNA sequence was identified using the amylase screening technique described in Example 2 above, wherein that cDNA sequence is designated herein as DNA24256 (Figure 205; SEQ ID NO:484). That cDNA sequence was then compared and aligned with other known EST sequencees as described in Example 1 above to obtain a consensus DNA sequence which is designated herein as DNA43422. Based on the DNA 43422 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO1083.

A pair of PCR primers (forward and reverse) were synthesized:

<u>forward PCR primer</u> 5'-GGCATTGGAGCAGTGCTGGGTG-3' (SEQ ID NO:485);

<u>reverse PCR primer</u> 5'-TGGAGGCCTAGATGCGGCTGGACG-3' (SEQ ID NO:486).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO1083 gene using the reverse PCR primer. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO1083 [herein designated as UNQ540 (DNA50921-1458)] (SEQ ID NO:482) and the derived protein sequence for PRO1083.

The entire nucleotide sequence of UNQ540 (DNA50921-1458) is shown in Figure 203 (SEQ ID NO:482). Clone UNQ540 (DNA50921-1458) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 214-216 and ending at the stop codon at nucleotide positions 2293-2295 (Figure 203). The predicted polypeptide precursor is 693 amino acids long (Figure 204). The full-length PRO1083 protein shown in Figure 204 has an estimated molecular weight of about 77,738 daltons and a pI of about 8.87. Clone UNQ540 (DNA50921-1458) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Still analyzing the amino acid sequence of SEQ ID NO:483, the putative signal peptide is at about amino acids 1-25 of SEQ ID NO:483. The transmembrane domains are at about amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590 and 634-657 of SEQ ID NO:483. A microbodies C-terminal targeting signal is at about amino acids 691-693 of SEQ ID NO:483. cAMP- and cGMP-dependent protein kinase phosphorylation sites are at about amino acids 198-201 and 370-373 of SEQ ID NO:483. N-glycosylation sites are at about amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-227 and 341-344 of SEQ ID NO:483. A G-protein coupled receptor family domain is at about amino acids 475-504 of SEQ ID NO:483. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 84: Isolation of cDNA Clones Encoding Human PRO200

Probes based on an expressed sequence tag (EST) identified from the Incyte Pharmaceuticals database due to homology with VEGF were used to screen a cDNA library derived from the human glioma cell line G61. In particular, Incyte Clone "INC1302516" was used to generate the following four probes:

(SEQ ID NO:489) ACTTCTCAGTGTCCATAAGGG;

(SEQ ID NO:490) GAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTC;

(SEQ ID NO:491) CACCACAGCGTTTAACCAGG; and

(SEQ ID NO:492) ACAACAGGCACAGTTCCCAC.

Nine positives were identified and characterized. Three clones contained the full coding region and were identical in sequence. Partial clones were also identified from a fetal lung library and were identical with the glioma-derived sequence with the exception of one nucleotide change which did not alter the encoded amino acid.

EXAMPLE 85: Expression Constructs for PRO200

For mammalian protein expression, the entire open reading frame (ORF) was cloned into a CMV-based expression vector. An epitope-tag (FLAG, Kodak) and Histidine-tag (His8) were inserted between the ORF and stop codon. VEGF-E-His8 and VEGF-E-FLAG were transfected into human embryonic kidney 293 cells by

SuperFect (Qiagen) and pulse-labeled for 3 hours with [^{35}S]methionine and [^{35}C]cysteine. Both epitope-tagged proteins co-migrate when 20 microliters of 15-fold concentrated serum-free conditioned medium were electrophoresed on a polyacrylamide gel (Novex) in sodium dodecyl sulfate sample buffer (SDS-PAGE). The VEGF-E-IgG expression plasmid was constructed by cloning the ORF in front of the human Fc (IgG) sequence.

The VEGF-E-IgG plasmid was co-transfected with Baculogold Baculovirus DNA (Pharmingen) using Lipofectin (GibcoBRL) into 10^5 Sf9 cells grown in Hink's TNM-FH medium (JRH Biosciences) supplemented with 10% fetal bovine serum. Cells were incubated for 5 days at 28°C. The supernatant was harvested and subsequently used for the first viral amplification by infecting Sf9 cells at an approximate multiplicity of infection (MOI) of 10. Cells were incubated for 3 days, then supernatant harvested, and expression of the recombinant plasmid determined by binding of 1 ml of supernatant to 30 μl of Protein-A Sepharose CL-4B beads (Pharmacia) followed by subsequent SDS-PAGE analysis. The first amplification supernatant was used to infect a 500 ml spinner culture of Sf9 cells grown in ESF-921 medium (Expression Systems LLC) at an approximate MOI of 0.1. Cells were treated as above, except harvested supernatant was sterile filtered. Specific protein was purified by binding to Protein-A Sepharose 4 Fast Flow (Pharmacia) column.

Example 86: Northern Blot Analyses for PRO200

Blots of human poly(A)+ RNA from multiple adult and fetal tissues and tumor cell lines were obtained from Clontech (Palo Alto, CA). Hybridization was carried out using ^{32}P-labeled probes containing the entire coding region and washed in 0.1 x SSC, 0.1% SDS at 63°C.

VEGF-E mRNA was detectable in fetal lung, kidney, brain, liver and adult heart, placenta, liver, skeletal muscle, kidney, and pancreas. VEGF-E mRNA was also found in A549 lung adenocarcinoma and HeLa cervical adenocarcinoma cell lines.

Example 87: In Situ Hybridization of Human Fetal Tissue Sections for PRO200

Formalin-fixed, paraffin-embedded human fetal brain, liver, lower limb, small intestine, thyroid, lymph node, thymus, stomach, trachea, skin, spleen, spinal cord, adrenal, placenta, cord, and adult liver, pancreas, lung, spleen, lymph node, adrenal, heart, aorta, and skin were sectioned, deparaffinized, deproteinated in proteinase K (20 μg/ml) for 15 minutes at 37°C, and further processed for in situ hybridization as described by Lu LH and Gillett NA (Cell Vision 1:169-176, 1994). A [α-^{33}-P]UTP-labeled antisense riboprobe was generated from a PCR product of 980 bp (primers GGCGGAATCCAACCTGAGTAG and GCGGCTATCCTCCTGTGCTC, SEQ ID NOS: 493 and 494, respectively). The slides were dipped in Kodak NTB2 nuclear track emulsion and exposed for 4 weeks.

VEGF-E mRNA expression included localization at the growth plate region and embracing fetal myocytes.

Example 88: Myocyte Hypertrophy Assay for PRO200

Myocytes from neonatal Harlan Sprague Dawley rat heart ventricle (23 days gestation) were plated in duplicate at 75000 cells/ml in a 96-well plate. Cells were treated for 48h with 2000, 200, 20, or 2 ng/ml VEGF-E-IgG. Myocytes were stained with crystal violet to visualize morphology and scored on a scale of 3 to 7, 3 being nonstimulated and 7 being full-blown hypertrophy.

2000 ng/ ml and 200 ng/ ml VEGF-E caused hypertrophy, scored as a 5.

Example 89: Cell Proliferation Assay for PRO200

Mouse embryonic fibroblast C3HIOT1/2 cells (ATCC) were grown in 50:50 Ham's F-12: low glucose DMEM medium containing 10% fetal calf serum (FCS). Cells were plated in duplicate in a 24-well plate at 1000, 2000, and 4000 cells/well. After 48 hours, cells were switched to medium containing 2% FCS and were incubated for 72 hours with 200, 800, or 2000 ng/ml VEGF-E or no growth factor added.

Approximately 1.5 fold greater number of cells were measured in the presence of 200 ng/ml VEGF-E as in its absence, at all three cell densities.

Example 90: Endothelial Cell Survival Assay for PRO200

Human umbilical vein endothelial cells (HUVEC, Cell Systems) were maintained in Complete Media (Cell Systems) and plated in triplicate in serum-free medium (Basic Media from Cell Systems containing 0.1% BSA) at 20,000 cells/well of a 48-well plate. Cells were incubated for 5 days with 200 or 400 ng/ml VEGF-E-IgG, 100 ng/ml VEGF, 20 ng/ml basic FGF, or no addition.

Survival was 2-3 times greater with VEGF-E as compared to lack of growth factor addition. VEGF and basic FGF were included as positive controls.

EXAMPLE 91: Isolation of cDNA Clones Encoding Human PRO285

A proprietary expressed sequence tag (EST) DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA) was searched and an EST (#2243209) was identified which showed homology to the *Drosophila* Toll protein.

Based on the EST, a pair of PCR primers (forward and reverse):

TAAAGACCCAGCTGTGACCG (SEQ ID NO:499)

ATCCATGAGCCTCTGATGGG (SEQ ID NO: 500), and

a probe:

ATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTC (SEQ ID NO: 501)

were synthesized.

mRNA for construction of the cDNA libraries was isolated from human placenta tissue. The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA (Fast Track 2). The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately

by gel electrophoresis, and cloned in a defined orientation into the cloning vector pCR2.1 (Invitrogen, Inc.) using reagents and protocols from Life Technologies, Gaithersburg, MD (Super Script Plasmid System). The double stranded cDNA was sized to greater than 1000 bp and the cDNA was cloned into BamHI/NotI cleaved vector. pCR2.1 is a commercially available plasmid, designed for easy cloning of PCR fragments, that carries AmpR and KanR genes for selection, and LacZ gene for blue-white selection.

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO285 gene using the probe oligonucleotide and one of the PCR primers.

A cDNA clone was sequenced in entirety. The entire nucleotide sequence of DNA40021-1154 (encoding PRO285) is shown in Figure 208 (SEQ ID NO:495). Clone DNA40021-1154 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 61-63 (Figure 208). The predicted polypeptide precursor is 1049 amino acids long, including a putative signal peptide at amino acid positions 1-29, a putative transmembrane domain between amino acid positions 837-860, and a leucine zipper pattern at amino acid positions 132-153 and 704-725, respectively. It is noted that the indicated boundaries are approximate, and the actual limits of the indicated regions might differ by a few amino acids. Clone DNA40021-1154 has been deposited with ATCC (designation: DNA40021-1154) and is assigned ATCC deposit no.209389.

Based on a BLAST and FastA sequence alignment analysis (using the ALIGN computer program) of the full-length sequence is a human analogue of the *Drosophila* Toll protein, and is homologous to the following human Toll proteins: Toll1 (DNAX# HSU88540-1, which is identical with the random sequenced full-length cDNA #HUMRSC786-1); Toll2 (DNAX# HSU88878-1); Toll3 (DNAX# HSU88879-1); and Toll4 (DNAX# HSU88880-1).

EXAMPLE 92: Isolation of cDNA Clones Encoding Human PRO286

A proprietary expressed sequence tag (EST) DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA) was searched and an EST (#694401) was identified which showed homology to the *Drosophila* Toll protein.

Based on the EST, a pair of PCR primers (forward and reverse):

GCCGAGACAAAAACGTTCTCC (SEQ ID NO:502)

CATCCATGTTCTCATCCATTAGCC (SEQ ID NO: 503), and

a probe:

TCGACAACCTCATGCAGAGCATCAACCAAAGCAAGAAAACAGTATT (SEQ ID NO: 504)

were synthesized.

mRNA for construction of the cDNA libraries was isolated from human placenta tissue. This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, MD (Super Script Plasmid System). pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased

adaptors, cleaved with NotI, sized to greater than 1000 bp appropriately by gel electrophoresis, and cloned in a defined orientation into XhoI/NotI-cleaved pRK5D.

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO286 gene using the probe oligonucleotide identified above and one of the PCR primers.

A cDNA clone was sequenced in entirety. The entire nucleotide sequence of DNA42663-1154 (encoding PRO286) is shown in Figures 210A-B (SEQ ID NO:497). Clone DNA42663-1154 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 57-59 (Figure 211). The predicted polypeptide precursor is 1041 amino acids long, including a putative signal peptide at amino acid positions 1-26, a potential transmembrane domain at amino acid positions 826-848, and leucine zipper patterns at amino acids 130-151, 206-227, 662-684, 669-690 and 693-614, respectively. It is noted that the indicated boundaries are approximate, and the actual limits of the indicated regions might differ by a few amino acids. Clone DNA42663-1154 has been deposited with ATCC (designation: DNA42663-1154) and is assigned ATCC deposit no. 209386.

Based on a BLAST and FastA sequence alignment analysis (using the ALIGN computer program) of the full-length sequence of PR0286, it is a human analogue of the *Drosophila* Toll protein, and is homologous to the following human Toll proteins: Toll1 (DNAX# HSU88540-1, which is identical with the random sequenced full-length cDNA #HUMRSC786-1); Toll2 (DNAX# HSU88878-1); Toll3 (DNAX# HSU88879-1); and Toll4 (DNAX# HSU88880-1).

<u>Example 93</u>: <u>NF-κB Assay for PRO285 and PRO286</u>

As the Toll proteins signal through the NF-κB pathway, their biological activity can be tested in an NF-κB assay. In this assay Jurkat cells are transiently transfected using Lipofectamine reagent (Gibco BRL) according to the manufacturer's instructions. 1μg pB2XLuc plasmid, containing NF-κB-driven luciferase gene, is contransfected with 1μg pSRαN expression vector with or without the insert encoding PRO285 or PRO286. For a positive control, cells are treated with PMA (phorbol myristyl acetate; 20 ng/ml) and PHA (phytohaemaglutinin, 2μg/ml) for three to four hours. Cells are lysed 2 or 3 days later for measurement of luciferase activity using reagents from Promega.

<u>EXAMPLE 94</u>: <u>Isolation of cDNA Clones Encoding Human PRO213-1, PRO1330 and PRO1449</u>

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA28735. Based on the DNA28735 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO213-1, PRO1330 and/or PRO1449. A pair of PCR primers (forward and reverse) were synthesized:

<u>forward PCR primer</u> 5'-TGGAGCAGCAATATGCCAGCC-3' (SEQ ID NO:511)

reverse PCR primer 5'-TTTTCCACTCCTGTCGGGTTGG-3' (SEQ ID NO:512)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA28735 sequence which had the following nucleotide sequence:

hybridization probe

5'-GGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGG-3' (SEQ ID NO:513)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO213-1, PRO1330 and/or PRO1449 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal lung tissue.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence encoding PRO213-1, PRO1330 and/or PRO1449 [DNA30943-1-1163-1 (SEQ ID NO:505), DNA64907-1163-1 (SEQ ID NO:507) and DNA64908-1163-1 (SEQ ID NO:509), respectively].

The entire nucleotide sequencescorresponding to DNA30943-1-1163-1 (SEQ ID NO:505), DNA64907-1163-1 (SEQ ID NO:507) and DNA64908-1163-1 (SEQ ID NO:509), respectively. DNA30943-1163, DNA64907-1163-1 and DNA64908-1163-1 contain a single open reading frame with an apparent translational initiation site at nucleotide positions 336-338, 488-490 and 326-328, respectively, and ending at the stop codon at nucleotide positions 1221-1223, 1307-1309 and 1145-1147, respectively (Figures 212, 214 and 216). The predicted polypeptide precursor is 295, 273 and 273 amino acids long, respectively (Figures 213, 215 and 217). DNA30943-1-1163-1, DNA64907-1163-1 and DNA64908-1163-1 have been deposited with ATCC and are assigned ATCC deposit no. 209791, 203242 and 203243, respectively.

Analysis of the amino acid sequence of the full-length PRO213-1 polypeptide suggests that a portion of it possess significant homology to the human growth arrest-specific gene 6 protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO213 amino acid sequence and the following Dayhoff sequences, HSMHC3W5A_6 and B48089.

Additional analysis of the amino acid sequence of the full-length PRO1330 and PRO1449 polypeptide indicates significant identity with notch4. More specifically, an analysis of the Dayhoff database (version 35.130 SwissProt 35) evidenced significant identity between PRO1330 and the following Dayhoff sequences, D86566_1 and NEL_HUMAN.

EXAMPLE 95: Isolation of cDNA Clones Encoding Human PRO298

A cDNA isolated in the amylase screen described in Example 2 above is herein designated DNA26832 (Figure 220; SEQ ID NO:516). The sequence of DNA26832 was then used to search expressed sequence tag (EST) databases. The EST databases included public EST databases (e.g., GenBank) and a proprietary EST database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266: 469-480 [1996]). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington,

Seattle, Washington; http://bozeman.mbt.washington.edu/phrap.docs/phrap.html).

A consensus DNA sequence was assembled relative to other EST sequences using phrap. A consensus sequence was determined, which was then extended using repeated cycles of BLAST and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above. The extended assembly sequence was designated DNA35861.Based on the DNA35861 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence of PRO298. Forward and reverse primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe sequence is typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel et al., Current Protocols in Molecular Biology, with the PCR primer pair. A positive library was used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

PCR primers (forward and reverse) and a hybridization probe were synthesized:

forward PCR primer 1 CAACGTGATTTCAAAGCTGGGCTC (SEQ ID NO:517)

forward PCR primer 2 GCCTCGTATCAAGAATTTCC (SEQ ID NO:518)

forward PCR primer 3 AGTGGAAGTCGACCTCCC (SEQ ID NO:519)

reverse PCR primer 1 CTCACCTGAAATCTCTCATAGCCC (SEQ ID NO:520)

hybridization probe 1 CGCAAAACCCATTTTGGGAGCAGGAATTCCAATCATGTCTGTGATGGTGG (SEQ ID NO:521)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO298 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal lung tissue (LIB25). The cDNA libraries used to isolated the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO298 (herein designated UNQ261 [DNA39975-1210]) (SEQ ID NO:514), and the derived protein sequence for PRO298 (SEQ ID NO:515).

The entire nucleotide sequence of UNQ261 (DNA39975-1210) is shown in Figure 218 (SEQ ID NO:514). Clone DNA39975-1210 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 375-377. The predicted polypeptide precursor is 364 amino acids long. The protein contains four putative transmembrane domains between amino acid positions 36-55 (type II TM), 65-84, 188-

208, and 229-245, respectively. A putative N-linked glycosylation site starts at amino acid position 253. In addition, the following features have been identified in the protein sequence: cAMP- and cGMP-dependent protein kinase phosphorylation site, starting at position 8; N-myristoylation sites starting a position 173 and 262, respectively; and a ZP domain between amino acid positions 45-60. Clone DNA39975-1210 has been deposited with ATCC (April 21, 1998) and is assigned ATCC deposit no.209783.

EXAMPLE 96: Isolation of cDNA Clones Encoding Human PRO337

A cDNA sequence identified in the amylase screen described in Example 2 above is herein designated DNA42301 (Figure 223, SEQ ID NO:524). The DNA42301 sequence was then compared to other EST sequences using phrap as described in Example 1 above and a consensus sequence designated herein as DNA28761 was identified. Based on this consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence. In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO337 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal brain.

A cDNA clone was sequenced in its entirety. The full length nucleotide sequence of DNA43316-1237 is shown in Figure 221 (SEQ ID NO:522). Clone DNA43316-1237 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 134-136 (Figure 221; SEQ ID NO:522). The predicted polypeptide precursor is 344 amino acids long. Clone DNA43316-1237 has been deposited with ATCC and is assigned ATCC deposit no. 209487

Based on a BLAST-2 and FastA sequence alignment analysis of the full-length sequence, PRO337 shows amino acid sequence identity to rat neurotrimin (97%).

EXAMPLE 97: Isolation of cDNA Clones Encoding Human PRO403

Introduction:

Human thrombopoietin (THPO) is a glycosylated hormone of 352 amino acids consisting of two domains. The N-terminal domain, sharing 50% similarity to erythropoietin, is responsible for the biological activity. The C-terminal region is required for secretion. The gene for thrombopoietin (THPO) maps to human chromosome 3q27-q28 where the six exons of this gene span 7 kilobase base pairs of genomic DNA (Chang et al., Genomics 26: 636-7 (1995); Foster et al., Proc. Natl. Acad. Sci. USA 91: 13023-7 (1994); Gurney et al., Blood 85: 981-988 (1995). In order to determine whether there were any genes encoding THPO homologues located in close proximity to THPO, genomic DNA fragments from this region were identified and sequenced. Three P1 clones and one PAC clones (Genome Systems Inc., St. Louis, MO; cat. Nos. P1-2535 and PAC-6539) encompassing the THPO locus were isolated and a 140 kb region was sequenced using the ordered shotgun strategy (Chen et al., Genomics 17: 651-656 (1993)), coupled with a PCR-based gap filling approach. Analysis reveals that the region is gene-rich with four additional genes located very close to THPO: tumor necrosis factor-

receptor type 1 associated protein 2 (TRAP2) and elongation initiation factor gamma (eIF4(), chloride channel 2 (CLCN2) and RNA polymerase II subunit hRPB17. While no THPO homolog was found in the region, four novel genes have been predicted by computer-assisted gene detection (GRAIL)(Xu et al., Gen. Engin. 16: 241-253 (1994), the presence of CpG islands (Cross, S. and Bird, A., Curr. Opin. Genet. & Devel. 5: 109-314 (1995), and homology to known genes (as detected by WU-BLAST2.0)(Altschul and Gish, Methods Enzymol. 266: 460-480 (1996) (http://blast.wustl.edu/blast/README.html).

Procedures:

P1 and PAC clones:

The initial human P1 clone was isolated from a genomic P1 library (Genome Systems Inc., St. Louis, MO; cat. no.: P1-2535) screened with PCR primers designed from the THPO genomic sequence (A.L. Gurney, et al., Blood 85: 981-88 (1995). PCR primers were designed from the end sequences derived from this P1 clone were then used to screen P1 and PAC libraries (Genome Systems, Cat. Nos.: P1-2535 & PAC-6539) to identify overlapping clones (PAC1, p1.t, and P1.u). The 3'-end sequence from PAC.z was used to define the primers used for the screening of a human BAC library (Genome Systems Inc., St. Louis, MO; Cat. No.: BDTW-4533A).

Ordered Shotgun Strategy:

The Ordered Shotgun Strategy (OSS) (Chen et al., Genomics 17: 651-656 (1993)) involves the mapping and sequencing of large genomic DNA clones with a hierarchical approach. The P1 or PAC clone was sonicated and the fragments subcloned into lambda vector (λBluestar) (Novagen, Inc., Madison, WI; cat. no. 69242-3). The lambda subclone inserts were isolated by long-range PCR (Barnes, W. Proc. Natl. Acad. Sci. USA 91: 2216-2220 (1994) and the ends sequenced. The lambda-end sequences were overlapped to create a partial map of the original clone. Those lambda clones with overlapping end-sequences were identified, the insets subcloned into a plasmid vector (pUC18 or pUC19, Hoefer Pharmacia Biotech, Inc., San Francisco, CA, Cat. Nos. 27-4949-01 and 27-4951-01) and the ends of the plasmid subclones were sequenced and assembled to generate a contiguous sequence. This directed sequencing strategy minimizes the redundancy required while allowing one to scan for and concentrate on interesting regions.

In order to define better the THPO locus and to search for other genes related to the hematopoietin family, five genomic clones were isolated from this region by PCR screening of human P1 and PAC libraries (Genome System, Inc., Cat. Nos.: P1-2535 and PAC-6539).

The sizes of the genomic fragments are as follows: P1.t is 40 kb; P1.g is 70 kb; P1.u is 70 kb; PAC.z is 200 kb; and BAC.1 is 80 kb. Approximately 75% (140 kb) of the 190 kb genomic DNA region was sequenced by the Ordered Shotgun Strategy (OSS) (Chen et al., Genomics 17: 651-56 (1993), and assembled into contigs using AutoAssemblerTM (Applied Biosystems, Perkin Elmer, Foster City, CA, cat. no. 903227). The preliminary order of these contigs was determined by manual analysis. There were 47 contigs the 140 kb region. A PCR-based approach to ordering the contigs and filling in the gaps was employed. The following summarizes the number and sizes of the gaps. The 50 kb of sequence unique to BAC.1 was sequenced by a total shotgun approach with a ten-fold redundancy.

Size of gap	number
<50 bp	13
50-150 bp	7
150-300 bp	7
300-1000 bp	10
1000-5000 bp	7
> 5000 bp	2 ((15,000 bp)

DNA sequencing:

ABI DYE-primerTM chemistry (PE Applied Biosystems, Foster City, CA; Cat. No.: 402112) was used to end-sequence the lambda and plasmid subclones. ABI DYE-terminaterTMchemistry (PE Applied Biosystems, Foster City, CA, Cat. No: 403044) was used to sequence the PCR products with their respective PCR primers. The sequences were collected with an ABI377 instrument. For PCR products larger than 1kb, walking primers were used. The sequences of contigs generated by the OSS strategy in AutoAssemblerTM (PE Applied Biosystems, Foster City, CA; Cat. No: 903227) and the gap-filling sequencing trace files were imported into SequencherTM (Gene Codes Corp., Ann Arbor, MI) for overlapping and editing. The sequences generated by the total shotgun strategy were assembled using Phred and Phrap and edited using Consed (http://chimera.biotech.washington.edu/uwgc/projects.htm) and GFP (Genome Reconstruction Manager for Phrap), version 1.2 (http://stork.cellb.bcm.tmc.edu/gfp/).

PCR-Based gap filling Strategy:

Primers were designed based on the 5'- and 3'-end sequenced of each contig, avoiding repetitive and low quality sequence regions. All primers were designed to be 19-24-mers with 50-70% G/C content. Oligos were synthesized and gel-purified by standard methods.

Since the orientation and order of the contigs were unknown, permutations of the primers were used in the amplification reactions. Two PCR kits were used: first, XL PCR kit (Perkin Elmer, Norwalk, CT; Cat. No.: N8080205), with extension times of approximately 10 minutes; and second, the Taq polymerase PCR kit (Qiagen Inc., Valencia, CA; Cat. No.: 201223) was used under high stringency conditions if smeared or multiple products were observed with the XL PCR kit. The main PCR product from each successful reaction was extracted from a 0.9% low melting agarose gel and purified with the Geneclean DNA Purification kit prior to sequencing.

Analysis:

The identification and characterization of coding regions was carried out as follows: First, repetitive sequences were masked using RepeatMasker (A.F.A. Smit & P. Green, http://ftp.genome.washington.edu/RM/RM_details.html)which screens DNA sequences in FastA format against a library of repetitive elements and returns a masked query sequence. Repeats not masked were identified by comparing the sequence to the GenBank database using WUBLAST2.0 [Altschul, S & Gish, W., Methods Enzymol. 266: 460-480 (1996); http://blast.wustl.edu/blast/README.html] and were masked manually.

Next, known genes were revealed by comparing the genomic regions against Genentech's protein database using the WUBLAST2.0 algorithm and then annotated by aligning the genomic and cDNA sequences for each gene, respectively, using a Needleman-Wunch (Needleman and Wunsch, J. Mol. Biol. 48: 443-453 (1970) algorithm to find regions of local identity between sequences. The strategy results in detection of all exons of the five known genes in the region, THPO, TRAP2, eIF4g, CLCN2 and hRPB17 (see below).

Known genes	Map position
eukaryotic translation initiation factor 4 gamma	3q27-qter
thrombopoietin	3q26-q27
chloride channel 2	3q26-qter
TNF receptor associated protein 2	not previously mapped
RNA polymerase II subunit hRPB17	not previously mapped

Finally, novel transcription units were predicted using a number of approaches. CpG islands (S. Cross & Bird, A., Curr. Opin. Genet. Dev. 5: 109-314 (1995) islands were used to define promoter regions and were identified as clusters of sites cleaved by enzymes recognizing GC-rich, 6 or 8-mer palindromic sequences (NotI, NarI, BssHII, XhoI. CpG islands are usually associated with promoter regions of genes. WUBLAST2.0 analysis of short genomic regions (10-20 kb) versus GenBank revealed matches to ESTs. The individual EST sequences (or where possible, their sequence chromatogram files) were retrieved and assembled with Sequencer to provide a theoretical cDNA sequence (DNA36443). GRAIL2 (ApoCom Inc., Knoxville, TN, command line version for the DEC alpha) was used to predict a novel exon. The five known genes in the region served as internal controls for the success of the GRAIL algorithm.

Isolation:

A partial endothelin converting enzyme-2 (ECE-2) cDNA clone was isolated by first splicing in silico the ECE-2 exons predicted in the genomic sequence to generate a putative sequence (DNA36443). An oligonucleotide probe: GAAGCAGTGCAGCCAGCAGTAGAGAGGCACCTGCTAAGA) (SEQ ID NO:530) was designed and used to screen a human fetal small intestine library (LIB110) and internal PCR primers (36443f1) (ECE2.f:ACGCAGCTGGAGCTGGTCTTAGCA) (SEQ ID NO:531) and (36443r1) (ECE2.r) (GGTACTGGACCCCTAGGGCCACAA) (SEQ ID NO:532) were used to confirm clones hybridizing to the probe prior to sequencing. One positive clone was obtained, however this cDNA (DNA49830) represented a partially spliced transcript containing appropriately spliced exons 1 through 6, followed by intron 6 sequence. The oligo dT primer annealed to a polyA-stretch within an Alu element present in intron 6. An additional ECE-2 cDNA fragment (DNA49831) was obtained by PCR from a human fetal kidney library (LIB227) with primers designed from the presumed cDNA sequence [36443f3: CCTCCCAGCCGAGACCAGTGG (SEQ ID NO:533) and 36443r2: GGTCCTATAAGGGCCAAGACC (SEQ ID NO:534)]. This PCR product extended from exon 13 into the 3' untranslated region in exon 18.

A full length endothelin converting enzyme 2 (ECE-2) cDNA clone (DNA55800-1263) was isolated from an oligo-dT-primed human fetal brain library. RNA from human fetal brain tissue (20 weeks gestation, #283005)(SRC175) was isolated by guanidine thiocyanate and 5 μg used to generate double stranded cDNA which was cloned into the vector pRK5E. The 3' -primer (pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT) (SEQ ID NO:535) and the 5 -linker (pCGGACGCGTGGGTCGA) (SEQ ID NO:536) were designed to introduce XhoI and NotI restriction sites. The library was screened with PCR primers [36443pcrf1: CGGCCGTGATGGCTGGTGACG (SEQ ID NO:537) and 36443r3: GGCAGACTCCTTCCTATGGG (SEQ ID NO:538)] designed from the partial human ECE-2 cDNA sequences (DNA49830 and DNA49831). PCR products were cloned into the vector pCR2.1-TOPO (Invitrogen Corp., Carlsbad, CA, Cat. No. K4500-01) and sequenced with DYE-terminator chemistry as described above.

EXAMPLE 98: Northern Blot and in situ RNA Hybridization Analysis for PRO403

Expression of PRO403 mRNA in human tissues was examined by Northern blot analysis. Human polyA+ RNA blots derived from human fetal and adult tissues (Clontech, Palo Alto, CA; Cat. Nos. 7760-1, 7756-1 and 7755-1) were hybridized to a [32P-α]dATP-labelled cDNA fragments from probe based on the full length PRO403 cDNA. Blots were incubated with the probes in hybridization buffer (5X SSPE; 2X Denhardt's solution; 100 mg/mL denatured sheared salmon sperm DNA; 50% formamide; 2% SDS) for 18 hours at 42°C, washed to high stringency (0.1XSSC, 0.1% SDS, 50°C) and autoradiographed. The blots were developed after overnight exposure by phosphorimager analysis (Fuji).

PRO403 mRNA transcripts were detected. Analysis of the expression pattern showed the strongest signal of the expected 3.3 kb transcript in adult brain (highest in the cerebellum, putamen, medulla, and temporal lobe, and lower in the cerebral cortex, occipital lobe and frontal lobe), spinal cord, lung and pancreas and higher levels of a 4.5 kb transcript in fetal brain and kidney.

EXAMPLE 99: Use of PRO Polypeptide-Encoding Nucleic Acid as Hybridization Probes

The following method describes use of a nucleotide sequence encoding a PRO polypeptide as a hybridization probe.

DNA comprising the coding sequence of of a PRO polypeptide of interest as disclosed herein may be employed as a probe or used as a basis from which to prepare probes to screen for homologous DNAs (such as those encoding naturally-occurring variants of the PRO polypeptide) in human tissue cDNA libraries or human tissue genomic libraries.

Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO polypeptide-encoding nucleic acid-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO polypeptide can then be identified using standard techniques known in the art.

EXAMPLE 100: Expression of PRO Polypeptides in *E. coli*

This example illustrates preparation of an unglycosylated form of a desired PRO polypeptide by recombinant expression in *E. coli*.

The DNA sequence encoding the desired PRO polypeptide is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the specific PRO polypeptide coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO polypeptide can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

PRO181, PRO195, PRO200, PRO237, PRO273, PRO540, PRO322, PRO1017, PRO938, PRO162, PRO1114, PRO827 and PRO1008 were expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding the PRO polypeptide was initially amplified using selected PCR primers. The primers contained restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences were then ligated into an expression vector, which was used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq). Transformants were first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 was reached. Cultures were then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g $(NH_4)_2SO_4$, 0.71 g sodium citrate·2H2O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as

110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM $MgSO_4$) and grown for approximately 20-30 hours at 30°C with shaking. Samples were removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets were frozen until purification and refolding.

E. coli paste from 0.5 to 1 L fermentations (6-10 g pellets) was resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution was stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution was centrifuged at 40,000 rpm in a Beckman Ultracentifuge for 30 min. The supernatant was diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. Depending the clarified extract was loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column was washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein was eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein were pooled and stored at 4°C. Protein concentration was estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins were refolded by diluting sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes were chosen so that the final protein concentration was between 50 to 100 micrograms/ml. The refolding solution was stirred gently at 4°C for 12-36 hours. The refolding reaction was quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution was filtered through a 0.22 micron filter and acetonitrile was added to 2-10% final concentration. The refolded protein was chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance were analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein were pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded PRO proteins were pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins were formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

EXAMPLE 101: Expression of PRO Polypeptides in Mammalian Cells

This example illustrates preparation of a glycosylated form of a desired PRO polypeptide by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector.

Optionally, the PRO polypeptide-encoding DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO polypeptide DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-PRO polypeptide.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 μg pRK5-PRO polypeptide DNA is mixed with about 1 μg DNA encoding the VA RNA gene [Thimmappaya et al., Cell, 31:543 (1982)] and dissolved in 500 μl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M $CaCl_2$. To this mixture is added, dropwise, 500 μl of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM $NaPO_4$, and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 μCi/ml ^{35}S-cysteine and 200 μCi/ml ^{35}S-methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, PRO polypeptide may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., Proc. Natl. Acad. Sci., 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μg pRK5-PRO polypeptide DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 μg/ml bovine insulin and 0.1 μg/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO polypeptide can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, PRO polypeptides can be expressed in CHO cells. The pRK5-PRO polypeptide can be transfected into CHO cells using known reagents such as $CaPO_4$ or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ^{35}S-methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO polypeptide can then be concentrated and purified by any selected method.

Epitope-tagged PRO polypeptide may also be expressed in host CHO cells. The PRO polypeptide may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO polypeptide

insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO polypeptide can then be concentrated and purified by any selected method, such as by Ni^{2+}-chelate affinity chromatography.

Stable expression in CHO cells was performed using the following procedure. The proteins were expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins were fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs were subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., *Current Protocols of Molecular Biology,* Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas *et al., Nucl. Acids Res.* 24: 9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA were introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect® (Quiagen), Dosper® or Fugene® (Boehringer Mannheim). The cells were grown and described in Lucas *et al.*, supra. Approximately 3×10^{-7} cells are frozen in an ampule for further growth and production as described below.

The ampules containing the plasmid DNA were thawed by placement into water bath and mixed by vortexing. The contents were pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant was aspirated and the cells were resuspended in 10 mL of selective media (0.2 μm filtered PS20 with 5% 0.2 μm diafiltered fetal bovine serum). The cells were then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells were transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, a 250 mL, 500 mL and 2000 mL spinners were seeded with 3×10^5 cells/mL. The cell media was exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in US Patent No. 5,122,469, issued June 16, 1992 was actually used. 3L production spinner is seeded at 1.2×10^6 cells/mL. On day 0, the cell number pH were determined. On day 1, the spinner was sampled and sparging with filtered air was commenced. On day 2, the spinner was sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion). Throughout the production, pH was adjusted as necessary to keep at around 7.2. After 10 days, or until viability dropped below 70%, the cell culture was harvested by centrifugtion and filtering through a 0.22 μm filter. The filtrate was either stored at 4°C or immediately loaded onto columns for purification.

For the poly-His tagged constructs, the proteins were purified using a Ni-NTA column (Qiagen). Before purification, imidazole was added to the conditioned media to a concentration of 5 mM. The conditioned media was pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column was washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein was subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc containing) constructs of were purified from the conditioned media as follows. The conditioned medium was pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column was washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein was immediately neutralized by collecting 1 ml fractions into tubes containing 275 μL of 1 M Tris buffer, pH 9. The highly purified protein was subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity was assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

The following PRO polypeptides were successfully transiently expressed in CHO cells: PRO200, PRO320, PRO237, PRO273, PRO337, PRO846, PRO363, PRO322, PRO1083, PRO938, PRO1012, PRO1114, PRO1008 and PRO1075.

The following PRO polypeptides were successfully transiently expressed in COS cells: PRO181, PRO195, PRO200, PRO320, PRO237, PRO273, PRO285, PRO337, PRO526, PRO540, PRO846, PRO362, PRO363, PRO700, PRO707, PRO617, PRO322, PRO719, PRO1083, PRO868, PRO866, PRO768, PRO938, PRO1012, PRO162, PRO1114, PRO827, PRO1008 and PRO1075.

The following PRO polypeptides were successfully stably expressed in CHO cells: PRO181, PRO195, PRO200, PRO320, PRO285, PRO337, PRO846, PRO362, PRO363, PRO707, PRO617, PRO322, PRO1083, PRO868, PRO866, PRO1017, PRO792, PRO788, PRO938, PRO1012, PRO162, PRO1114, PRO827, PRO1008, PRO1075 and PRO1031.

EXAMPLE 102: Expression of PRO Polypeptides in Yeast

The following method describes recombinant expression of a desired PRO polypeptide in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO polypeptides from the ADH2/GAPDH promoter. DNA encoding a desired PRO polypeptide, a selected signal peptide and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of the PRO polypeptide. For secretion, DNA encoding the PRO polypeptide can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, the yeast alpha-factor secretory signal/leader sequence, and linker sequences (if needed) for expression of the PRO polypeptide.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with

Coomassie Blue stain.

Recombinant PRO polypeptide can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing the PRO polypeptide may further be purified using selected column chromatography resins.

EXAMPLE 103: Expression of PRO Polypeptides in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO polypeptides in Baculovirus-infected insect cells.

The desired PRO polypeptide is fused upstream of an epitope tag contained with a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the PRO polypeptide or the desired portion of the PRO polypeptide (such as the sequence encoding the extracellular domain of a transmembrane protein) is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4-5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression is performed as described by O'Reilley et al., Baculovirus expression vectors: A laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO polypeptide can then be purified, for example, by Ni^{2+}-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert *et al., Nature*, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM $MgCl_2$; 0.1 mM EDTA; 10% Glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% Glycerol, pH 7.8) and filtered through a 0.45 μm filter. A Ni^{2+}-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A_{280} with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% Glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A_{280} baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or western blot with Ni^{2+}-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His $_{10}$-tagged PRO polypeptide are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO polypeptide can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

PRO195, PRO526, PRO540, PRO846, PRO362, PRO363, PRO700, PRO707, PRO322, PRO719, PRO1083, PRO868, PRO866, PRO768, PRO788, PRO938, PRO827 and PRO1031 were successfully expressed in baculovirus infected Sf9 insect cells. While the expression was actually performed in a 0.5-2 L scale, it can be readily scaled up for larger (e.g. 8 L) preparations. The proteins were expressed as an IgG construct (immunoadhesin), in which the protein extracellular region was fused to an IgG1 constant region sequence containing the hinge, CH2 and CH3 domains and/or in poly-His tagged forms.

For expression in baculovirus infected Sf9 cells, following PCR amplification, the respective coding sequences were subcloned into a baculovirus expression vector (pb.PH.IgG for IgG fusions and pb.PH.His.c for poly-His tagged proteins), and the vector and Baculogold® baculovirus DNA (Pharmingen) were co-transfected into 105 *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711), using Lipofectin (Gibco BRL). pb.PH.IgG and pb.PH.His are modifications of the commercially available baculovirus expression vector pVL1393 (Pharmingen), with modified polylinker regions to include the His or Fc tag sequences. The cells were grown in Hink's TNM-FH medium supplemented with 10% FBS (Hyclone). Cells were incubated for 5 days at 28°C. The supernatant was harvested and subsequently used for the first viral amplification by infecting Sf9 cells in Hink's TNM-FH medium supplemented with 10% FBS at an approximate multiplicity of infection (MOI) of 10. Cells were incubated for 3 days at 28°C. The supernatant was harvested and the expression of the constructs in the baculovirus expression vector was determined by batch binding of 1 ml of supernatant to 25 mL of Ni-NTA beads (QIAGEN) for histidine tagged proteins or Protein-A Sepharose CL-4B beads (Pharmacia) for IgG tagged proteins followed by SDS-PAGE analysis comparing to a known concentration of protein standard by Coomassie blue staining.

The first viral amplification supernatant was used to infect a spinner culture (500 ml) of Sf9 cells grown in ESF-921 medium (Expression Systems LLC) at an approximate MOI of 0.1. Cells were incubated for 3 days at 28°C. The supernatant was harvested and filtered. Batch binding and SDS-PAGE analysis was repeated, as necessary, until expression of the spinner culture was confirmed.

The conditioned medium from the transfected cells (0.5 to 3 L) was harvested by centrifugation to remove the cells and filtered through 0.22 micron filters. For the poly-His tagged constructs, the protein construct were purified using a Ni-NTA column (Qiagen). Before purification, imidazole was added to the conditioned media to a concentration of 5 mM. The conditioned media were pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column was washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein was subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc containing) constructs of proteins were purified from the conditioned media as follows. The conditioned media were pumped onto a 5 ml Protein A column (Pharmacia) which had been

equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column was washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein was immediately neutralized by collecting 1 ml fractions into tubes containing 275 mL of 1 M Tris buffer, pH 9. The highly purified protein was subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity of the proteins was verified by SDS polyacrylamide gel (PEG) electrophoresis and N-terminal amino acid sequencing by Edman degradation.

PRO181, PRO195, PRO200, PRO320, PRO237, PRO273, PRO285, PRO337, PRO526, PRO540, PRO846, PRO362, PRO363, PRO617, PRO322, PRO1083, PRO868, 768, PRO792, PRO788, PRO162, PRO1114, PRO827, PRO1075 and PRO1031 were successfully expressed in baculovirus infected Hi5 insect cells. While the expression was actually performed in a 0.5-2 L scale, it can be readily scaled up for larger (e.g. 8 L) preparations.

For expression in baculovirus-infected Hi5 insect cells, the PRO polypeptide-encoding DNA may be amplified with suitable systems, such as Pfu (Stratagene), or fused upstream (5'-of) of an epitope tag contained with a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the PRO polypeptide or the desired portion of the PRO polypeptide (such as the sequence encoding the extracellular domain of a transmembrane protein) is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector. For example, derivatives of pVL1393 can include the Fc region of human IgG (pb.PH.IgG) or an 8 histidine (pb.PH.His) tag downstream (3'-of) the NAME sequence. Preferably, the vector construct is sequenced for confirmation.

Hi5 cells are grown to a confluency of 50% under the conditions of, 27°C, no CO2, NO pen/strep. For each 150 mm plate, 30 ug of pIE based vector containing PRO polypeptide is mixed with 1 ml Ex-Cell medium (Media: Ex-Cell 401 + 1/100 L-Glu JRH Biosciences #14401-78P (note: this media is light sensitive)), and in a separate tube, 100 ul of CellFectin (CellFECTIN (GibcoBRL #10362-010) (vortexed to mix)) is mixed with 1 ml of Ex-Cell medium. The two solutions are combined and allowed to incubate at room temperature for 15 minutes. 8 ml of Ex-Cell media is added to the 2ml of DNA/CellFECTIN mix and this is layered on Hi5 cells that have been washed once with Ex-Cell media. The plate is then incubated in darkness for 1 hour at room temperature. The DNA/CellFECTIN mix is then aspirated, and the cells are washed once with Ex-Cell to remove excess CellFECTIN. 30 ml of fresh Ex-Cell media is added and the cells are incubated for 3 days at 28°C. The supernatant is harvested and the expression of the PRO polypeptide in the baculovirus expression vector can be determined by batch binding of 1 ml of supernatent to 25 mL of Ni-NTA beads (QIAGEN) for histidine tagged proteins or Protein-A Sepharose CL-4B beads (Pharmacia) for IgG tagged proteins followed by SDS-PAGE analysis comparing to a known concentration of protein standard by Coomassie blue staining.

The conditioned media from the transfected cells (0.5 to 3 L) is harvested by centrifugation to remove the cells and filtered through 0.22 micron filters. For the poly-His tagged constructs, the protein comprising

the PRO polypeptide is purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently deslated into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc containing) constructs of proteins are purified from the conditioned media as follows. The conditioned media is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 mL of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity of PRO polypeptide can be assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation and other analytical procedures as desired or necessary.

EXAMPLE 104: Preparation of Antibodies that Bind to PRO Polypeptides

This example illustrates preparation of monoclonal antibodies which can specifically bind to a PRO polypeptide.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified PRO polypeptide, fusion proteins containing the PRO polypeptide, and cells expressing recombinant PRO polypeptide on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the PRO polypeptide immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO polypeptide antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO polypeptide. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against the PRO polypeptide. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against the PRO polypeptide is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO polypeptide monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 105: Chimeric PRO Polypeptides

PRO polypeptides may be expressed as chimeric proteins with one or more additional polypeptide domains added to facilitate protein purification. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS™ extension/affinity purification system (Immunex Corp., Seattle Wash.). The inclusion of a cleavable linker sequence such as Factor XA or enterokinase (Invitrogen, San Diego Calif.) between the purification domain and the PRO polypeptide sequence may be useful to facilitate expression of DNA encoding the PRO polypeptide.

EXAMPLE 106: Purification of PRO Polypeptides Using Specific Antibodies

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may

be secreted in useful quantity into the medium in which the cells are grown.

A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (*e.g.*, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (*e.g.*, a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

EXAMPLE 107: Drug Screening

This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (I) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

EXAMPLE 108: Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson, Bio/Technology, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of an PRO polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, Biochemistry, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, J. Biochem., 113:742-746 (1993).

It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

EXAMPLE 109: Ability of PRO Polypeptides to Inhibit Vascular Endothelial Growth Factor (VEGF) Stimulated Proliferation of Endothelial Cell Growth

The ability of various PRO polypeptides to inhibit VEGF stimulated proliferation of endothelial cells was tested. Specifically, bovine adrenal cortical capillary endothelial (ACE) cells (from primary culture, maximum 12-14 passages) were plated on 96-well microtiter plates (Amersham Life Science) at a density of 500 cells/well per 100 μL in low glucose DMEM, 10% calf serum, 2 mM glutamine, 1x pen/strept and fungizone, supplemented with 3 ng/mL VEGF. Controls were plated the same way but some did not include VEGF. A test sample of the PRO polypeptide of interest was added in a 100 μl volume for a 200 μl final volume. Cells were incubated for 6-7 days at 37°C. The media was aspirated and the cells washed 1x with PBS. An acid

phosphatase reaction mixture (100 μL, 0.1M sodium acetate, pH 5.5, 0.1% Triton-100, 10 mM p-nitrophenyl phosphate) was added. After incubation for 2 hours at 37°C, the reaction was stopped by addition of 10 μl 1N NaOH. OD was measured on microtiter plate reader at 405 nm. Controls were no cells, cells alone, cells + FGF (5 ng/mL), cells + VEGF (3 ng/mL), cells + VEGF (3 ng/ml) + TGF-β (1 ng/ml), and cells + VEGF (3ng/mL) + LIF (5 ng/mL). (TGF-β at a 1 ng/ml concentration is known to block 70-90% of VEGF stimulated cell proliferation.)

The results were assessed by calculating the percentage inhibition of VEGF (3 ng/ml) stimulated cells proliferation, determined by measuring acid phosphatase activity at OD405 nm, (1) relative to cells without stimulation, and (2) relative to the reference TGF-β inhibition of VEGF stimulated activity. The results are indicative of the utility of the PRO polypeptides in cancer therapy and specifically in inhibiting tumor angiogenesis.

The PRO polypeptides demonstrated as being capable of inhibiting VEGF stimulated proliferation of endothelial cell growth at various concentrations include PRO200 and PRO320.

EXAMPLE 110: Retinal Neuron Survival

This example demonstrates that various PRO polypeptides have efficacy in enhancing the survival of retinal neuron cells.

Sprague Dawley rat pups at postnatal day 7 (mixed population: glia and retinal neuronal types) are killed by decapitation following CO_2 anesthesia and the eyes are removed under sterile conditions. The neural retina is dissected away from the pigment epithelium and other ocular tissue and then dissociated into a single cell suspension using 0.25% trypsin in Ca^{2+}, Mg^{2+}-free PBS. The retinas are incubated at 37°C for 7-10 minutes after which the trypsin is inactivated by adding 1 ml soybean trypsin inhibitor. The cells are plated at 100,000 cells per well in 96 well plates in DMEM/F12 supplemented with N2 and with or without the specific test PRO polypeptide. Cells for all experiments are grown at 37°C in a water saturated atmosphere of 5% CO_2. After 2-3 days in culture, cells are stained with calcein AM then fixed using 4% paraformaldehyde and stained with DAPI for determination of total cell count. The total cells (fluorescent) are quantified at 20X objective magnification using CCD camera and NIH image software for MacIntosh. Fields in the well are chosen at random.

The effect of various concentration of PRO polypeptides is calculated by dividing the total number of calcein AM positive cells at 2-3 days in culture by the total number of DAPI-labeled cells at 2-3 days in culture. Anything above 30% survival is considered positive. The following PRO polypeptides were positive in this assay: PRO200, PRO540, PRO846 and PRO617.

EXAMPLE 111: Rod Photoreceptor Survival

This example demonstrates that various PRO polypeptides have efficacy in enhancing the survival of rod photoreceptor cells.

Sprague Dawley rat pups at 7 day postnatal (mixed population: glia and retinal neuronal cell types) are

killed by decapitation following CO_2 anesthesis and the eyes are removed under sterile conditions. The neural retina is dissected away form the pigment epithelium and other ocular tissue and then dissociated into a single cell suspension using 0.25% trypsin in Ca^{2+}, Mg^{2+}-free PBS. The retinas are incubated at 37°C for 7-10 minutes after which the trypsin is inactivated by adding 1 ml soybean trypsin inhibitor. The cells are plated at 100,000 cells per well in 96 well plates in DMEM/F12 supplemented with N2 and with or without the specific test PRO polypeptide. Cells for all experiments are grown at 37°C in a water saturated atmosphere of 5% CO2. After 2-3 days in culture, cells are fixed using 4% paraformaldehyde, and then stained using CellTracker Green CMFDA. Rho 4D2 (ascites or IgG 1:100), a monoclonal antibody directed towards the visual pigment rhodopsin is used to detect rod photoreceptor cells by indirect immunofluorescence. The results are reported as % survival: total number of calcein/CellTracker - rhodopsin positive cells at 2-3 days in culture, divided by the total number of rhodopsin positive cells at time 2-3 days in culture. The total cells (fluorescent) are quantified at 20x objective magnification using a CCD camera and NIH image software for MacIntosh. Fields in the well are chosen at random.

With regard to the effect of various concentration of PRO polypeptides, anything above 10% survival is considered positive. The following PRO polypeptides tested positive in this assay: PRO200, PRO540, PRO846 and PRO617.

EXAMPLE 112: <u>Ability of PRO Polypeptides to Stimulate the Release of Proteoglycans from Cartilage</u>

The ability of various PRO polypeptides to stimulate the release of proteoglycans from cartilage tissue was tested as follows.

The metacarphophalangeal joint of 4-6 month old pigs was aseptically dissected, and articular cartilage was removed by free hand slicing being careful to avoid the underlying bone. The cartilage was minced and cultured in bulk for 24 hours in a humidified atmosphere of 95% air, 5% CO_2 in serum free (SF) media (DME/F12 1:1) woth 0.1% BSA and 100U/ml penicillin and 100μg/ml streptomycin. After washing three times, approximately 100 mg of articular cartilage was aliquoted into micronics tubes and incubated for an additional 24 hours in the above SF media. PRO polypeptides were then added at 1% either alone or in combination with 18 ng/ml interleukin-1α, a known stimulator of proteoglycan release from cartilage tissue. The supernatant was then harvested and assayed for the amount of proteoglycans using the 1,9-dimethyl-methylene blue (DMB) colorimetric assay (Farndale and Buttle, <u>Biochem. Biophys. Acta</u> 883:173-177 (1985)). A positive result in this assay indicates that the test polypeptide will find use, for example, in the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis.

When PRO200 polypeptides were tested in the above assay, the polypeptides demonstrated a marked ability to stimulate release of proteoglycans from cartilage tissue both basally and after stimulation with interleukin-1α and at 24 and 72 hours after treatment, thereby indicating that PRO200 polypeptides are useful for stimulating proteoglycan release from cartilage tissue.

EXAMPLE 113: In Vitro Antiproliferative Assay

The antiproliferative activity of various PRO polypeptides was determined in the investigational, disease-oriented *in vitro* anti-cancer drug discovery assay of the National Cancer Institute (NCI), using a sulforhodamine B (SRB) dye binding assay essentially as described by Skehan et al., *J. Natl. Cancer Inst.* 82:1107-1112 (1990). The 60 tumor cell lines employed in this study ("the NCI panel"), as well as conditions for their maintenance and culture *in vitro* have been described by Monks et al., *J. Natl. Cancer Inst.* 83:757-766 (1991). The purpose of this screen is to initially evaluate the cytotoxic and/or cytostatic activity of the test compounds against different types of tumors (Monks et al., *supra*; Boyd, *Cancer: Princ. Pract. Oncol. Update* 3(10):1-12 [1989]).

Cells from approximately 60 human tumor cell lines were harvested with trypsin/EDTA (Gibco), washed once, resuspended in IMEM and their viability was determined. The cell suspensions were added by pipet (100 μL volume) into separate 96-well microtiter plates. The cell density for the 6-day incubation was less than for the 2-day incubation to prevent overgrowth. Inoculates were allowed a preincubation period of 24 hours at 37°C for stabilization. Dilutions at twice the intended test concentration were added at time zero in 100 μL aliquots to the microtiter plate wells (1:2 dilution). Test compounds were evaluated at five half-log dilutions (1000 to 100,000-fold). Incubations took place for two days and six days in a 5% CO_2 atmosphere and 100% humidity.

After incubation, the medium was removed and the cells were fixed in 0.1 ml of 10% trichloroacetic acid at 40°C. The plates were rinsed five times with deionized water, dried, stained for 30 minutes with 0.1 ml of 0.4% sulforhodamine B dye (Sigma) dissolved in 1% acetic acid, rinsed four times with 1% acetic acid to remove unbound dye, dried, and the stain was extracted for five minutes with 0.1 ml of 10 mM Tris base [tris(hydroxymethyl)aminomethane], pH 10.5. The absorbance (OD) of sulforhodamine B at 492 nm was measured using a computer-interfaced, 96-well microtiter plate reader.

A test sample is considered positive if it shows at least 50% growth inhibitory effect at one or more concentrations. The following PRO polypeptides gave positive results in at least one tumor cell line: PRO181, PRO237, PRO526, PRO362 and PRO866.

EXAMPLE 114: Gene Amplification

This example shows that genes encoding various PRO polypeptides are amplified in the genome of certain human cancers. Amplification is associated with overexpression of the gene product, indicating that the PRO polypeptide is a useful target for therapeutic intervention in certain cancers such as colon, lung and other cancers. Therapeutic agent may take the form of antagonists of PRO polypeptide-encoding genes, for example, murine-human chimeric, humanized or human antibodies against the PRO polypeptide.

The starting material for the screen was genomic DNA isolated from a variety cancers. The DNA is quantitated precisely, e.g., fluorometrically. As a negative control, DNA was isolated from the cells of ten normal healthy individuals which was pooled and used as assay controls for the gene copy in healthy individuals (NorHu).

The 5' nuclease assay (for example, TaqMan™) and real-time quantitative PCR (for example, ABI Prizm 7700 Sequence Detection System™ (Perkin Elmer, Applied Biosystems Division, Foster City, CA)), were used to find genes potentially amplified in certain cancers. The results were used to determine whether the DNA encoding the PRO polypeptide is over-represented in any of the lung and colon cancers that were screened. The result was reported in Delta CT units. One unit corresponds 1 PCR cycle or approximately a 2-fold amplification relative to normal, two units corresponds to 4-fold, 3 units to 8-fold and so on. Quantitation was obtained using primers and a Taqman™ fluorescent derived from the PRO polypeptide-encoding gene. Regions of the PRO polypeptide which are most likely to contain unique nucleic acid sequences and which are least likely to have spliced out introns are preferred for the primer derivation, e.g., 3'-untranslated region.

The 5' nuclease assay reaction is a fluorescent PCR-based technique which makes use of the 5' exonuclease activity of Taq DNA polymerase enzyme to monitor amplification in real time. Two oligonucleotide primers are used to generate an amplicon typical of a PCR reaction. A third oligonucleotide, or probe, is designed to detect nucleotide sequence located between the two PCR primers. The probe is non-extendible by Taq DNA polymerase enzyme, and is labeled with a reporter fluorescent dye and a quencher fluorescent dye. Any laser-induced emission from the reporter dye is quenched by the quenching dye when the two dyes are located close together as they are on the probe. During the amplification reaction, the probe is cleaved by the Taq DNA polymerase enzyme in a template-dependent manner. The resultant probe fragments disassociate in solution, and signal from the released reporter dye is free from the quenching effect of the second fluorophore. One molecule of reporter dye is liberated for each new molecule synthesized, and detection of the unquenched reporter dye provides the basis for quantitative interpretation of the data.

The 5' nuclease procedure is run on a real-time quantitative PCR device such as the ABI Prism 7700TM Sequence Detection. The system consists of a thermocyler, laser, charge-coupled device (CCD) camera and computer. The system amplifies samples in a 96-well format on a thermocycler. During amplification, laser-induced fluorescent signal is collected in real-time through fiber optics cables for all 96 wells, and detected at the CCD. The system includes software for running the intrument and for analyzing the data.

5' Nuclease assay data are initially expressed as Ct, or the threshold cycle. This is defined as the cycle at which the reporter signal accumulates above the background level of fluorescence. The Ct values are used as quantitative measurement of the relative number of starting copies of a particular target sequence in a nucleic acid sample.

Genes encoding the following PRO polypeptides were found to be amplified in the above assay: PRO213-1, PRO237, PRO324, PRO351, PRO362, PRO853, PRO615, PRO531, PRO618, PRO772, PRO703, PRO474, PRO1017 and PRO792.

EXAMPLE 115: Induction of c-fos in Endothelial Cells

Human venous umbilical vein endothelial cells (HUVEC, Cell Systems) in growth media (50:50 without glycine, 1% glutamine, 10mM Hepes, 10% FBS, 10 ng/ml bFGF), were plated on 96-well microtiter plates at a cell density of 1×10^4 cells/well. The day after plating, the cells were starved by removing the growth media

and treating the cells with 100 μl/well test samples and controls (positive control: growth media; negative control: Protein 32). The cells were incubated for 30 minutes at 37°C, in 5% CO_2. The samples were removed, and the first part of the bDNA kit protocol (Chiron Diagnostics, cat. #6005-037) was followed.

Briefly, the amounts of the TM Lysis Buffer and Probes needed for the tests were calculated based on information provided by the manufacturer. The appropriate amounts of thawed Probes were added to the TM Lysis Buffer. The Capture Hybridization Buffer was warmed to room temperature. The bDNA strips were set up in the metal strip holders, and 100 μl of Capture Hybridization Buffer were added to each b-DNA well needed, followed by incubation for at least 30 minutes. The test plates with the cells were removed from the incubator, and the media was gently removed using the vacuum manifold. 100μl of Lysis Hybridization Buffer with Probes were quickly pipetted into each well of the microtiter plates. The plates were then incubated at 55°C for 15 minutes. Upon removal from the incubator, the plates were placed on the vortex mixer with the microtiter adapter head and vortex on the #2 setting for one minute. 80 μl of the lysate were removed and added to the bDNA wells containing the Capture Hybridization Buffer, and pipetted up and down to mix. The plates were incubated at 53°C for at least 16 hours.

On the next day, the second part of the bDNA kit protocol was followed. Specifically, the Plates were removed from the incubator and placed on the bench to cool for 10 minutes. The volumes of additions needed were calculated based upon information provided by the manufacturer. An Amplifier Working Solution was prepared by making a 1:100 dilution of the Amplifier Concentrate (20 fm/μl) in AL Hybridization Buffer. The hybridization mixture was removed from the plates and washed twice with Wash A. 50 μl of Amplifier Working Solution were added to each well and the wells were incubated at 53°C for 30 minutes. The plates were then removed from the incubator and allowed to cool for 10 minutes. The Label Probe Working Solution was prepared by making a 1:100 dilution of Label Concentrate (40 pmoles/μl) in AL Hybridization Buffer. After the 10 minutes cool down period, the amplifier hybridization mixture was removed and the plates washed twice with Wash A. 50μl of Label Probe Working Solution were added to each well and the wells were incubated at 53°C for 15 minutes. After cooling for 10 minutes, the Substrate was warmed to room temperature. Upon addition of 3 μl of Substrate Enhancer to each ml of Substrate needed for the assay, the plates were allowed to cool for 10 minutes, the label hybridization mixture was removed, and the plates were washed twice with Wash A and three-times with Wash D. 50μl of the Substrate Solution with Enhancer were added to each well. The plates were incubated for 30 minutes at 37°C and RLU read in an appropriate luminometer.

The replicates were averaged and the coefficient of variation was determined. The measure of activity of the fold increase over the Protein 32 (buffer control) value indicated by chemoluminescence units (RLU). Samples which showed an at least two-fold value over the Protein 32 value were considered positive. PRO938 was positive in the above assay.

EXAMPLE 116: Proliferation of Rat Utricular Supporting Cells

In an effort to identify PRO polypeptides that act as potent mitogens for inner ear supporting cells which are hair cell progenitors (related to auditory hair cell regeneration), various PRO polypeptides were tested in the

following assay.

The rat utricular epithelial cell line (UEC-4 cells) are aliquoted into 96 well plates with a density of 3000 cells/well in 200 μl of serum-containing medium at 33°C. After overnight, the cultures are switched to serum-free medium at 37°C and the PRO polypeptide samples are added at various dilutions. After 24h incubation, ^{3}H-thymidine (1 μCi/well) is aded to the cultures for an additional 24h. The cells are then harvested using a Tomtec cell harvester. Because the epithelial cells are grown on a polylysine substrate, trypsin (1 mg/ml) is added to the culture wells for 30 min at 37°C to lift the cells before cell harvest. Cpm/well are counted with a matrix 9600 gas counter (Packard Instrument Company, Downers Grove, IL). Data is collected from 3 culture wells from each of the experimental groups and expressed as mean ± SEM. A two-tailed, unpaired t-test is used for statistical analysis, as compared to the control group (treatment with TGF-α).

Average cpm counts which are at least 30% higher than the control values are considered positive for the assay. The following PRO polypeptides were positive in this assay: PRO337, PRO363 and PRO1012.

EXAMPLE 117: *In situ* Hybridization

In situ hybridization is a powerful and versatile technique for the detection and localization of nucleic acid sequences within cell or tissue preparations. It may be useful, for example, to identify sites of gene expression, analyze the tissue distribution of transcription, identify and localize viral infection, follow changes in specific mRNA synthesis and aid in chromosome mapping.

In situ hybridization was performed following an optimized version of the protocol by Lu and Gillett, Cell Vision 1:169-176 (1994), using PCR-generated ^{33}P-labeled riboprobes. Briefly, formalin-fixed, paraffin-embedded human tissues were sectioned, deparaffinized, deproteinated in proteinase K (20 g/ml) for 15 minutes at 37°C, and further processed for *in situ* hybridization as described by Lu and Gillett, *supra*. A [^{33}-P] UTP-labeled antisense riboprobe was generated from a PCR product and hybridized at 55°C overnight. The slides were dipped in Kodak NTB2 nuclear track emulsion and exposed for 4 weeks.

^{33}P-Riboprobe synthesis

6.0 μl (125 mCi) of ^{33}P-UTP (Amersham BF 1002, SA<2000 Ci/mmol) were speed vac dried. To each tube containing dried ^{33}P-UTP, the following ingredients were added:

2.0 μl 5x transcription buffer

1.0 μl DTT (100 mM)

2.0 μl NTP mix (2.5 mM : 10 μ; each of 10 mM GTP, CTP & ATP + 10 μl H_2O)

1.0 μl UTP (50 μM)

1.0 μl Rnasin

1.0 μl DNA template (1μg)

1.0 μl H_2O

1.0 μl RNA polymerase (for PCR products T3 = AS, T7 = S, usually)

The tubes were incubated at 37°C for one hour. 1.0 μl RQ1 DNase were added, followed by incubation at 37°C for 15 minutes. 90 μl TE (10 mM Tris pH 7.6/1mM EDTA pH 8.0) were added, and the mixture was

pipetted onto DE81 paper. The remaining solution was loaded in a Microcon-50 ultrafiltration unit, and spun using program 10 (6 minutes). The filtration unit was inverted over a second tube and spun using program 2 (3 minutes). After the final recovery spin, 100 μl TE were added. 1 μl of the final product was pipetted on DE81 paper and counted in 6 ml of Biofluor II.

The probe was run on a TBE/urea gel. 1-3 μl of the probe or 5 μl of RNA Mrk III were added to 3 μl of loading buffer. After heating on a 95°C heat block for three minutes, the gel was immediately placed on ice. The wells of gel were flushed, the sample loaded, and run at 180-250 volts for 45 minutes. The gel was wrapped in saran wrap and exposed to XAR film with an intensifying screen in -70°C freezer one hour to overnight.

^{33}P-Hybridization

A. Pretreatment of frozen sections

The slides were removed from the freezer, placed on aluminium trays and thawed at room temperature for 5 minutes. The trays were placed in 55°C incubator for five minutes to reduce condensation. The slides were fixed for 10 minutes in 4% paraformaldehyde on ice in the fume hood, and washed in 0.5 x SSC for 5 minutes, at room temperature (25 ml 20 x SSC + 975 ml SQ H_2O). After deproteination in 0.5 μg/ml proteinase K for 10 minutes at 37°C (12.5 μl of 10 mg/ml stock in 250 ml prewarmed RNase-free RNAse buffer), the sections were washed in 0.5 x SSC for 10 minutes at room temperature. The sections were dehydrated in 70%, 95%, 100% ethanol, 2 minutes each.

B. Pretreatment of paraffin-embedded sections

The slides were deparaffinized, placed in SQ H_2O, and rinsed twice in 2 x SSC at room temperature, for 5 minutes each time. The sections were deproteinated in 20 μg/ml proteinase K (500 μl of 10 mg/ml in 250 ml RNase-free RNase buffer; 37°C, 15 minutes) - human embryo, or 8 x proteinase K (100 μl in 250 ml Rnase buffer, 37°C, 30 minutes) - formalin tissues. Subsequent rinsing in 0.5 x SSC and dehydration were performed as described above.

C. Prehybridization

The slides were laid out in a plastic box lined with Box buffer (4 x SSC, 50% formamide) - saturated filter paper. The tissue was covered with 50 μl of hybridization buffer (3.75g Dextran Sulfate + 6 ml SQ H_2O), vortexed and heated in the microwave for 2 minutes with the cap loosened. After cooling on ice, 18.75 ml formamide, 3.75 ml 20 x SSC and 9 ml SQ H_2O were added, the tissue was vortexed well, and incubated at 42°C for 1-4 hours.

D. Hybridization

1.0 x 10^6 cpm probe and 1.0 μl tRNA (50 mg/ml stock) per slide were heated at 95°C for 3 minutes. The slides were cooled on ice, and 48 μl hybridization buffer were added per slide. After vortexing, 50 μl ^{33}P mix were added to 50 μl prehybridization on slide. The slides were incubated overnight at 55°C.

E. Washes

Washing was done 2 x 10 minutes with 2xSSC, EDTA at room temperature (400 ml 20 x SSC + 16 ml 0.25M EDTA, V_f=4L), followed by RNaseA treatment at 37°C for 30 minutes (500 μl of 10 mg/ml in 250

ml Rnase buffer = 20 μg/ml). The slides were washed 2 x 10 minutes with 2 x SSC, EDTA at room temperature. The stringency wash conditions were as follows: 2 hours at 55°C, 0.1 x SSC, EDTA (20 ml 20 x SSC + 16 ml EDTA, V_f=4L).

F. Oligonucleotides

In situ analysis was performed on a variety of DNA sequences disclosed herein. The oligonucleotides employed for these analyses were derived from the nucleotide sequences disclosed herein and generally range from about 40 to 55 nucleotides in length.

G. Results

In situ analysis was performed on a variety of DNA sequences disclosed herein. The results from these analyses are as follows.

(1) DNA29101-1122 (PRO200)

Fetal: Lower limb expression in developing lower limb bones at the edge of the cartilagenous anlage (i.e. around the outside edge); in developing tendons, in vascular smooth muscle and in cells embracing developing skeletal muscle myocytes and myotubes. Expression also observed at the epiphyseal growth plate. Lymph node expression in marginal sinus of developing lymph nodes. Thymus expression in the subcapsular region of the thymic cortex, possibly representing either the subcapsular epithelial cells or the proliferating, double negative, thymocytes that are found in this region. Spleen is negative. Trachea expression in smooth muscle. Brain (cerebral cortex) focal expression in cortical neurones. Spinal cord negative. Small intestine expression in smooth muscle. Thyroid - generalized expression over thyroid epithelium. Adrenal is negative. Liver expression in ductal plate cells. Stomach expression in mural smooth muscle. Fetal skin expression in basal layer of squamous epithelium. Placenta expression in interstitial cells in trophoblastic villi. Cord expression in wall of arteries and vein.

Comments: Expression pattern suggests that PRO200 may be involved in cell differentiation/proliferation.

High expression was observed at the following additional sites: Chimp ovary - granulosa cells of maturing follicles, lower intensity signal observed over thecal cells. Chimp parathyroid - high expression over chief cells. Human fetal testis - moderate expression over stromal cells surrounding developing tubules. Human fetal lung - high expression over chondrocytes in developing bronchial tree, and low level expression over branching bronchial epithelium. Specific expression was not observed over the renal cell, gastric and colonic carcinomas. Fetal tissues examined (E12-E16 weeks) include: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb. Adult tissues examined: liver, kidney, adrenal, myocardium, aorta, spleen, lymph node, pancreas, lung, skin, cerebral cortex (rm), hippocampus(rm), cerebellum(rm), penis, eye, bladder, stomach, gastric carcinoma, colon, colonic carcinoma and chondrosarcoma. Acetominophen induced liver injury and hepatic cirrhosis.

(2) DNA30867-1335 (PRO218)

Low level expression over numerous epithelia including fetal small intestine, fetal thyroid, chimp gastric epithelium. Expression also seen over malignant cells in a renal cell carcinoma. Expression in fetal brain, over cortex. The distribution does not suggest an obvious function. Human fetal tissues examined (E12-E16 weeks) include: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb. Adult human tissues examined: kidney (normal and end-stage), bladder, adrenal, spleen, lymph node, pancreas, lung, skin, eye (inc. retina), colon, bladder, liver (normal, cirrhotic, acute failure), heart, clear cell carcinoma of kidney, gastric adenocarcinoma, colorectal carcinoma. Non-human primate tissues examined: Chimp tissues: salivary gland, stomach, thyroid, parathyroid, tongue, thymus, ovary, lymph node, peripheral nerve. Rhesus Monkey tissues: cerebral cortex, hippocampus, cerebellum, penis.

(3) DNA40021-1154 (PRO285)

Low levels of expression observed in the placenta and over hematopoietic cells in the mouse fetal liver. No expression was detected in either human fetal, adult or chimp lymph node and no expression was detected in human fetal or human adult spleen. Fetal tissues examined (E12-E16 weeks) include: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb. Adult tissues examined: liver, kidney, adrenal, myocardium, aorta, spleen, lymph node, pancreas, lung, skin, cerebral cortex (rm), hippocampus(rm), cerebellum(rm), brain infarct (human), cerebritis (human),penis, eye, bladder, stomach, gastric carcinoma, colon, colonic carcinoma, thyroid (chimp), parathyroid (chimp) ovary (chimp) and chondrosarcoma. Acetominophen induced liver injury and hepatic cirrhosis.

(4) DNA39523-1192 (PRO273)

Expression over epithelium of mouse embryo skin as well as over basal epithelium and dermis of human fetal skin. Basal epithelial pegs of the squamous mucosa of the chimp tongue are also positive. Expression over a subset of cells in developing glomeruli of fetal kidney, adult renal tubules, and over "thyroidized" epithelium in end-stage renal disease, low expression in a renal cell carcinoma, probably over the epithelial cells. Low level expression over stromal cells in fetal lung. Expression over stromal cells in the apical portion of gastric glands. High expression in the lamina propria of the fetal small intestinal villi, normal colonic mucosa and over stromal cells in a colonic carcinoma. Strong expression over benign connective tissue cells in the hylanized stroma of a sarcoma. Expression over stromal cells in the placental villi and the splenic red pulp. In the brain, expression over cortical neurones. Connective tissue surrounding developing bones and over nerve sheath cells in the fetus. Fetal tissues examined (E12-E16 weeks) include: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb. Adult tissues examined: liver, kidney, adrenal, myocardium, aorta, spleen, lymph node, pancreas, lung, skin, cerebral cortex (rm), hippocampus(rm), eye, stomach, gastric

carcinoma, colon, colonic carcinoma, thyroid (chimp), parathyroid (chimp) ovary (chimp) and chondrosarcoma. Acetominophen induced liver injury and hepatic cirrhosis.

Expression was present in many cells in the outer layers (I and II) of the monkey cerebral cortex. A small subset of cells in the deeper cortical layers also expressed mRNA for this chemokine homolog. Scattered cells within the molecular layers of the hippocampus and bordering the inner edge of the dentate gyrus contained chemokine homolog mRNA. No expression was detected within the cerebellar cortex. Chemokine homolog expression is not observed in infarcted brain, where cell death has occurred in the regions where the chemokine homolog normally is expressed. This probe could possibly serve as a marker of a subset of neurons of outer layers of the cerebral cortex and could possibly reveal neuronal migration disorders. Abnormal neuronal migration is a possible cause of some seizure disorders and schizophrenia. In order to gain a better appreciation of the distribution of this mRNA we will test whether the probe will cross-hybridize with mouse brain tissue.

Also shows intriguing and specific patterns of hybridization within postnatal day (P)10 and adult mouse brains. In one sagittal section of P10 mouse brain, strong signal was observed scattered within the molecular layer of the hippocampus and inner edges of the dentate gyrus. Cells in the presubiculum were moderately labeled; the signal extended in a strong band through outer layers of the retrosplenial cortes to the occipital cortex, where the signal diminished to background levels. A small set of positive neurons were detected in deeper regions of P10 motor cortex; neurons in outer layers of P10 cortex did not exhibit signal above background levels. Moderate hybridization signal was also detected in the inferior colliculus. Chemokine homolog signal in the adult mouse brain was evaluated in three coronal sections at different levels. Strong signal was detected in the septum and in scattered neurons in the pontine nuclei and motor root of the trigeminal nerve; moderate signal was seen in the molecular layers of the hippocampus and outer layers of the retrosplenial cortex.

(5) <u>DNA39979-1213 (PRO296)</u>

Widespread expression in fetal in adult tissues. Expressed in a variety of fetal and adult epithelia, skeletal and cardiac muscle, developing (including retina) and adult CNS, thymic epithelium, placental villi, hepatocytes in cirrhotic and acetaminophen induced toxicity. Highly expressed in hypertrophic chondrocytes in developing skeletal system.The overall expression pattern, while not completely ovelapping (not expressed in glomeruli, more widely expressed in CNS), is not disimilar to VEGF. A possible role in angiogenesis should therefore be considered. Human fetal tissues examined (E12-E16 weeks) include: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, great vessels, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis, testis and lower limb. Adult human tissues examined: kidney (normal and end-stage), adrenal, spleen, lymph node, pancreas, lung, eye (inc. retina), bladder, liver (normal, cirrhotic, acute failure). Non-human primate tissues examined: Chimp tissues: adrenal. Rhesus Monkey tissues: cerebral cortex, hippocampus, cerebellum.

(6) DNA52594-1270 (PRO868)

Expression over neuronal cells in fetal dorsal root ganglia, spinal cord, developing enteric neurons, cortical neurons. Low level expression also seen in placental trophoblast. In adult tissues the only site where notable expression was observed was the normal adult prostate; as such it may represent a possible prostate cell surface receptor target antigen. Studies to further characterize the expression in adult tissues seem warranted. Low level expression also observed in a liposarcoma. Fetal tissues examined (E12-E16 weeks) include: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb. Adult human tissues examined: liver, kidney, adrenal, myocardium, aorta, spleen, lung, skin, chondrosarcoma, eye, stomach, gastric carcinoma, colon, colonic carcinoma, renal cell carcinoma, prostate, bladder mucosa and gall bladder. Acetominophen induced liver injury and hepatic cirrhosis. Rhesus tissues examined: cerebral cortex (rm), hippocampus(rm), cerebellum. Chimp tissues examined: thyroid, parathyroid, ovary, nerve, tongue, thymus, adrenal, gastric mucosa and salivary gland. WIG-1(WISP-1), WIG-2 (WISP-2) and WIG-5 (WISP-3) expression in human breast carcinoma and normal breast tissue, Wig-2 in lung carcinoma, and Wig-5 in colon carcinoma.

(7) DNA64907-1163 (PRO1330)

In human fetal tissues there was strong specific expression over artrerial, venous, capillary and sinusoidal endothelium in all tissues examined, except for fetal brain. In normal adult tissues expression was low to absent, but when present appeared expression was confined to the vasculature. Highest expression in adult tissues was observed regionally in vessels running within the white matter of rhesus brain - the significance of this pattern is unclear. Elevated expression observed in vasculature of many inflamed and diseased tissues, including tumor vasculature. In some of these tissues it was unclear if expression was soley confined to vascular endothelium. In the 15 lung tumors examined no expression was seen over the malignant epithelium, however, vascular expression was observed in many of the tumors and adjacent lung tissue. Moderate, apparently non-specific background, was seen with this probe over hyalinised collagen and sites of tissue necrosis. In the abscence of a sense control, however, it is not possible to be absolutely certain that all of this signal is non-specific. Some signal, also thought to be non-specific, was seen over the chimp gastric mucosa, transitional cell epithelium of human adult bladder and fetal retina.

(8) DNA49624-1279 (PRO545)

Expression of the ADAM family molecule, ADAM 12 (DNA49624-1279) observed in normal human lung, lung tumor, normal colon and colon carcinoma.

(9) DNA59294-1381 (PRO1031)

The expression of this IL17 homologue was evaluated in a panel consisting of normal adult and fetal tissues and tissues with inflammation, predominantly chronic lymphocytic inflammation. This panel is designed to specifically evaluate the expression pattern in immune mediated inflammatory disease of novel proteins that

modulate T lymphocyte function (stimulatory or inhibitory). This protein when expressed as an Ig-fusion protein was immunostimulatory in a dose dependent fashion in the human mixed lymphocyte reaction (MLR); it caused a 285% and 147% increase above the baseline stimulation index when utilized at two different concentrations (1.0% and 0.1% of a 560 nM stock). Summary: expression was restricted to muscle, certain types of smooth muscle in the adult and in skeletal and smooth muscle in the human fetus.. Expression in adult human was in smooth muscle of tubular organs evaluated including colon and gall bladder. There no expression in the smooth muscle of vessels or bronchi. No adult human skeletal muscle was evaluated. In fetal tissues there was moderate to high diffuse expression in skeletal muscle the axial skeleton and limbs. There was weak expression in the smooth muscle of the intestinal wall but no expression in cardiac muscle. Adult human tissues with expression: Colon. there was low level diffuse expression in the smooth muscle (tunica muscularis) in 5 specimens with chronic inflammatory bowel disease. Gall bladder: there was weak to low level expression in the smooth muscle of the gall bladder. Fetal human tissues with expression: there was moderate diffuse expression in skeletal muscle and weak tolow expression in smooth muscle; there was no expression in fetal heart or any other fetal organ including liver, spleen, CNS, kidney, gut, lung. Human tissues with no expression: lung with chronic granulomatous inflammation and chronic bronchitis (5 patients), peripheral nerve, prostate, heart, placenta, liver (disease multiblock), brain (cerbrum and cerebellum), tonsil (reactive hyperplasia), peripheral lymph node, thymus.

(10) <u>DNA45416-1251 (PRO362)</u>

The expression of this novel protein was evaluated in a variety of human and non-human primate tissues and was found to be highly restricted. Expression was present only in alveolar macrophages in the lung and in Kupffer cells of the hepatic sinusoids. Expression in these cells was significantly increased when these distinct cell populations were activated. Though these two subpopulations of tissue macrophages are located in different organs, they have similar biological functions. Both types of these phagocytes act as biological filters to remove material from the blood stream or airways including pathogens, senescent cells and proteins and both are capable of secreting a wide variery of important proinflammatory cytokines. In inflamed lung (7 patient samples) expression was prominent in reactive alveolar macrophage cell populations defined as large, pale often vacuolated cells present singly or in aggregates within alveoli and was weak to negative in normal, non-reactive macrophages (single scattered cells of normal size). Expression in alveolar macrophages was increased during inflammation when these cells were both increased in numbers and size (activated). Despite the presence of histocytes in areas of interstial inflammtion and peribronchial lymphoid hyperplasia in these tissues, expression was restricted to alveolar macrophages. Many of the inflamed lungs also had some degree of suppurative inflammation; expression was not present in neutrophilic granulocytes. In liver, there was strong expression in reactive/activated Kupffer cells in livers with acute centrilobular necrosis (acetominophen toxicity) or fairly marked periportal inflammtion. However there was weak or no expression in Kupffer cells in normal liver or in liver with only mild inflammation or mild to moderate lobular hyperplasia/hypertrophy. Thus, as in the lung, there was increased expression in acivated/reative cells. There was no expression of this molecule in histiocytes/macropahges present in inflamed bowel, hyperplastic/reactive tonsil or normal lymph node. The lack

of expression in these tissues which all contained histiocytic inflammation or resident macrophage populations strongly supports restricted expression to the unique macrophage subset populations defined as alveolar macrophage and hepatic Kupffer cells. Spleen or bone marrow was not available for evaluation. Human tissues evaluated which had no detectable expression included: Inflammatory bowel disease (7 patient samples with moderate to severe disease), tonsil with reactive hyperplasia, peripheral lymphnode, psoriatic skin (2 patient samples with mild to moderate disease), heart, peripheral nerve. Chimp tissues evaluated which had no detectable expression included: tongue, stomach, thymus.

(11) DNA52196-1348 (PRO733)

Generalized low level signal in many tissues and in many cell types. While endothelial cell expression was observed it was not a prominent feature in either fetal, normal or diseased tissues. Human tissues: moderate expression over fetal liver (mainly hepatocytes), lung, skin, adrenal and heart. Fetal spleen, small intestine, brain and eye are negative. Adult normal kidney, bladder epithelium, lung, adrenal, pancreas, skin - all negative. Expression in adult human liver (normal and diseased), renal tubules in end-stage renal disease, adipose tissue, sarcoma, colon, renal cell carcinoma, hepatocellular carcinoma, squamous cell carcinoma. Non human primate tissues: chimp salivary gland, vessels, stomach, tongue, peripheral nerve, thymus, lymph node, thyroid and parathyroid. Rhesus spinal cord negative, cortical and hippocampal neurones positive.

Deposit of Material

The following materials have been deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD, USA (ATCC):

Material	ATCC Dep. No.	Deposit Date
DNA39987-1184	ATCC 209786	April 21, 1998
DNA40625-1189	ATCC 209788	April 21, 1998
DNA23318-1211	ATCC 209787	April 21, 1998
DNA39979-1213	ATCC 209789	April 21, 1998
DNA40594-1233	ATCC 209617	February 5, 1998
DNA45416-1251	ATCC 209620	February 5, 1998
DNA45419-1252	ATCC 209616	February 5, 1998
DNA52594-1270	ATCC 209679	March 17, 1998
DNA45234-1277	ATCC 209654	March 5, 1998
DNA49624-1279	ATCC 209655	March 5, 1998
DNA48309-1280	ATCC 209656	March 5, 1998
DNA46776-1284	ATCC 209721	March 31, 1998
DNA50980-1286	ATCC 209717	March 31, 1998
DNA50913-1287	ATCC 209716	March 31, 1998
DNA50914-1289	ATCC 209722	March 31, 1998
DNA48296-1292	ATCC 209668	March 11, 1998
DNA32284-1307	ATCC 209670	March 11, 1998
DNA36343-1310	ATCC 209718	March 31, 1998
DNA40571-1315	ATCC 209784	April 21, 1998
DNA41386-1316	ATCC 209703	March 26, 1998
DNA44194-1317	ATCC 209808	April 28, 1998
DNA45415-1318	ATCC 209810	April 28, 1998

DNA44189-1322	ATCC 209699	March 26, 1998
DNA48304-1323	ATCC 209811	April 28, 1998
DNA49152-1324	ATCC 209813	April 28, 1998
DNA49646-1327	ATCC 209705	March 26, 1998
DNA49631-1328	ATCC 209806	April 28, 1998
DNA49645-1347	ATCC 209809	April 28, 1998
DNA45493-1349	ATCC 209805	April 28, 1998
DNA48227-1350	ATCC 209812	April 28, 1998
DNA41404-1352	ATCC 209844	May 6, 1998
DNA44196-1353	ATCC 209847	May 6, 1998
DNA52187-1354	ATCC 209845	May 6, 1998
DNA48328-1355	ATCC 209843	May 6, 1998
DNA56352-1358	ATCC 209846	May 6, 1998
DNA53971-1359	ATCC 209750	April 7, 1998
DNA50919-1361	ATCC 209848	May 6, 1998
DNA44179-1362	ATCC 209851	May 6, 1998
DNA54002-1367	ATCC 209754	April 7, 1998
DNA53906-1368	ATCC 209747	April 7, 1998
DNA52185-1370	ATCC 209861	May 14, 1998
DNA53977-1371	ATCC 209862	May 14, 1998
DNA57253-1382	ATCC 209867	May 14, 1998
DNA58847-1383	ATCC 209879	May 20, 1998
DNA58747-1384	ATCC 209868	May 14, 1998
DNA57689-1385	ATCC 209869	May 14, 1998
DNA23330-1390	ATCC 209775	April 14, 1998
DNA26847-1395	ATCC 209772	April 14, 1998
DNA53974-1401	ATCC 209774	April 14, 1998
DNA57039-1402	ATCC 209777	April 14, 1998
DNA57033-1403	ATCC 209905	May 27, 1998
DNA34353-1428	ATCC 209855	May 12, 1998
DNA45417-1432	ATCC 209910	May 27, 1998
DNA39523-1192	ATCC 209424	October 31, 1997
DNA44205-1285	ATCC 209720	March 31, 1998
DNA50911-1288	ATCC 209714	March 31, 1998
DNA48329-1290	ATCC 209785	April 21, 1998
DNA48306-1291	ATCC 209911	May 27, 1998
DNA48336-1309	ATCC 209669	March 11, 1998
DNA44184-1319	ATCC 209704	March 26, 1998
DNA48314-1320	ATCC 209702	March 26, 1998
DNA48333-1321	ATCC 209701	March 26, 1998
DNA50920-1325	ATCC 209700	March 26, 1998
DNA50988-1326	ATCC 209814	April 28, 1998
DNA48331-1329	ATCC 209715	March 31, 1998
DNA30867-1335	ATCC 209807	April 28, 1998
DNA55737-1345	ATCC 209753	April 7, 1998
DNA49829-1346	ATCC 209749	April 7, 1998
DNA52196-1348	ATCC 209748	April 7, 1998
DNA56965-1356	ATCC 209842	May 6, 1998
DNA56405-1357	ATCC 209849	May 6, 1998
DNA57530-1375	ATCC 209880	May 20, 1998
DNA56439-1376	ATCC 209864	May 14, 1998
DNA56409-1377	ATCC 209882	May 20, 1998
DNA56112-1379	ATCC 209883	May 20, 1998
DNA56045-1380	ATCC 209865	May 14, 1998
DNA59294-1381	ATCC 209866	May 14, 1998

DNA56433-1406	ATCC 209857	May 12, 1998
DNA53912-1457	ATCC 209870	May 14, 1998
DNA50921-1458	ATCC 209859	May 12, 1998
DNA29101-1122	ATCC 209653	March 5, 1998
DNA40021-1154	ATCC 209389	October 17, 1997
DNA42663-1154	ATCC 209386	October 17, 1997
DNA30943-1-1163-1	ATCC 209791	April 21, 1998
DNA64907-1163-1	ATCC 203242	September 9, 1998
DNA64908-1163-1	ATCC 203243	September 9, 1998
DNA39975-1210	ATCC 209783	April 21, 1998
DNA43316-1237	ATCC 209487	November 21, 1997
DNA55800-1263	ATCC 209680	March 17, 1998

These deposit were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

WHAT IS CLAIMED IS:

1. Isolated nucleic acid having at least 80% sequence identity to a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132), Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150), Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270), Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375), Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523) and Figure 225 (SEQ ID NO:526).

2. The nucleic acid sequence of Claim 1, wherein said nucleotide sequence comprises a nucleotide sequence selected from the group consisting of the sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:6), Figure 8 (SEQ ID NO:18), Figure 10 (SEQ ID NO:27), Figure 14 (SEQ ID NO:35), Figure 19 (SEQ ID NO:44), Figure 21 (SEQ ID NO:51), Figure 23 (SEQ ID NO:58), Figure 25 (SEQ ID NO:63), Figure 27 (SEQ ID NO:68), Figure 29 (SEQ ID NO:73), Figure 32 (SEQ ID NO:84), Figure 34 (SEQ ID NO:89), Figure 36 (SEQ ID NO:96), Figure 38 (SEQ ID NO:101), Figure 40 (SEQ ID NO:108), Figure 42 (SEQ ID NO:113), Figure 44 (SEQ ID NO:118), Figure 46 (SEQ ID NO:123), Figure 48 (SEQ ID NO:131), Figure 50 (SEQ ID

NO:136), Figure 52 (SEQ ID NO:144), Figure 54 (SEQ ID NO:149), Figure 58 (SEQ ID NO:156), Figure 60 (SEQ ID NO:161), Figure 62 (SEQ ID NO:168), Figure 65 (SEQ ID NO:177), Figure 67 (SEQ ID NO:182), Figure 69 (SEQ ID NO:189), Figure 72 (SEQ ID NO:195), Figure 74 (SEQ ID NO:205), Figure 76 (SEQ ID NO:210), Figure 78 (SEQ ID NO:215), Figure 80 (SEQ ID NO:220), Figure 82 (SEQ ID NO:225), Figure 84 (SEQ ID NO:230), Figure 86 (SEQ ID NO:235), Figure 88 (SEQ ID NO:244), Figure 90 (SEQ ID NO:253), Figure 92 (SEQ ID NO:258), Figure 94 (SEQ ID NO:263), Figure 97 (SEQ ID NO:269), Figure 108 (SEQ ID NO:283), Figure 117 (SEQ ID NO:295), Figure 119 (SEQ ID NO:300), Figure 121 (SEQ ID NO:302), Figure 124 (SEQ ID NO:308), Figure 128 (SEQ ID NO:321), Figure 131 (SEQ ID NO:329), Figure 135 (SEQ ID NO:336), Figure 138 (SEQ ID NO:345), Figure 141 (SEQ ID NO:351), Figure 144 (SEQ ID NO:357), Figure 146 (SEQ ID NO:362), Figure 148 (SEQ ID NO:369), Figure 150 (SEQ ID NO:374), Figure 152 (SEQ ID NO:379), Figure 154 (SEQ ID NO:384), Figure 156 (SEQ ID NO:389), Figure 158 (SEQ ID NO:394), Figure 160 (SEQ ID NO:399), Figure 162 (SEQ ID NO:404), Figure 164 (SEQ ID NO:409), Figure 166 (SEQ ID NO:414), Figure 168 (SEQ ID NO:419), Figure 170 (SEQ ID NO:424), Figure 172 (SEQ ID NO:429), Figure 176 (SEQ ID NO:436), Figure 178 (SEQ ID NO:441), Figure 180 (SEQ ID NO:446), Figure 182 (SEQ ID NO:451), Figure 184 (SEQ ID NO:453), Figure 186 (SEQ ID NO:455), Figure 189 (SEQ ID NO:458), Figure 191 (SEQ ID NO:463), Figure 193 (SEQ ID NO:465), Figure 195 (SEQ ID NO:467), Figure 197 (SEQ ID NO:469), Figure 199 (SEQ ID NO:471), Figure 201 (SEQ ID NO:476), Figure 203 (SEQ ID NO:482), Figure 206 (SEQ ID NO:487), Figure 208 (SEQ ID NO:495), Figure 210 (SEQ ID NO:497), Figure 212 (SEQ ID NO:505), Figure 214 (SEQ ID NO:507), Figure 216 (SEQ ID NO:509), Figure 218 (SEQ ID NO:514), Figure 221 (SEQ ID NO:522) and Figure 224 (SEQ ID NO:525).

3. The nucleic acid of Claim 1, wherein said nucleotide sequence comprises a nucleotide sequence selected from the group consisting of the full-length coding sequence of the sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:6), Figure 8 (SEQ ID NO:18), Figure 10 (SEQ ID NO:27), Figure 14 (SEQ ID NO:35), Figure 19 (SEQ ID NO:44), Figure 21 (SEQ ID NO:51), Figure 23 (SEQ ID NO:58), Figure 25 (SEQ ID NO:63), Figure 27 (SEQ ID NO:68), Figure 29 (SEQ ID NO:73), Figure 32 (SEQ ID NO:84), Figure 34 (SEQ ID NO:89), Figure 36 (SEQ ID NO:96), Figure 38 (SEQ ID NO:101), Figure 40 (SEQ ID NO:108), Figure 42 (SEQ ID NO:113), Figure 44 (SEQ ID NO:118), Figure 46 (SEQ ID NO:123), Figure 48 (SEQ ID NO:131), Figure 50 (SEQ ID NO:136), Figure 52 (SEQ ID NO:144), Figure 54 (SEQ ID NO:149), Figure 58 (SEQ ID NO:156), Figure 60 (SEQ ID NO:161), Figure 62 (SEQ ID NO:168), Figure 65 (SEQ ID NO:177), Figure 67 (SEQ ID NO:182), Figure 69 (SEQ ID NO:189), Figure 72 (SEQ ID NO:195), Figure 74 (SEQ ID NO:205), Figure 76 (SEQ ID NO:210), Figure 78 (SEQ ID NO:215), Figure 80 (SEQ ID NO:220), Figure 82 (SEQ ID NO:225), Figure 84 (SEQ ID NO:230), Figure 86 (SEQ ID NO:235), Figure 88 (SEQ ID NO:244), Figure 90 (SEQ ID NO:253), Figure 92 (SEQ ID NO:258), Figure 94 (SEQ ID NO:263), Figure 97 (SEQ ID NO:269), Figure 108 (SEQ ID NO:283), Figure 117 (SEQ ID NO:295), Figure 119 (SEQ ID NO:300), Figure 121 (SEQ ID NO:302), Figure 124 (SEQ ID NO:308), Figure 128 (SEQ ID NO:321), Figure 131 (SEQ ID NO:329), Figure 135 (SEQ ID NO:336), Figure 138 (SEQ ID NO:345), Figure 141 (SEQ ID NO:351), Figure

144 (SEQ ID NO:357), Figure 146 (SEQ ID NO:362), Figure 148 (SEQ ID NO:369), Figure 150 (SEQ ID NO:374), Figure 152 (SEQ ID NO:379), Figure 154 (SEQ ID NO:384), Figure 156 (SEQ ID NO:389), Figure 158 (SEQ ID NO:394), Figure 160 (SEQ ID NO:399), Figure 162 (SEQ ID NO:404), Figure 164 (SEQ ID NO:409), Figure 166 (SEQ ID NO:414), Figure 168 (SEQ ID NO:419), Figure 170 (SEQ ID NO:424), Figure 172 (SEQ ID NO:429), Figure 176 (SEQ ID NO:436), Figure 178 (SEQ ID NO:441), Figure 180 (SEQ ID NO:446), Figure 182 (SEQ ID NO:451), Figure 184 (SEQ ID NO:453), Figure 186 (SEQ ID NO:455), Figure 189 (SEQ ID NO:458), Figure 191 (SEQ ID NO:463), Figure 193 (SEQ ID NO:465), Figure 195 (SEQ ID NO:467), Figure 197 (SEQ ID NO:469), Figure 199 (SEQ ID NO:471), Figure 201 (SEQ ID NO:476), Figure 203 (SEQ ID NO:482), Figure 206 (SEQ ID NO:487), Figure 208 (SEQ ID NO:495), Figure 210 (SEQ ID NO:497), Figure 212 (SEQ ID NO:505), Figure 214 (SEQ ID NO:507), Figure 216 (SEQ ID NO:509), Figure 218 (SEQ ID NO:514), Figure 221 (SEQ ID NO:522) or Figure 224 (SEQ ID NO:525).

4. Isolated nucleic acid which comprises the full-length coding sequence of the DNA deposited under accession number ATCC 209791, ATCC 209786, ATCC 209788, ATCC 209787, ATCC 209789, ATCC 209617, ATCC 209620, ATCC 209616, ATCC 209679, ATCC 209654, ATCC 209655, ATCC 209656, ATCC 209721, ATCC 209717, ATCC 209716, ATCC 209722, ATCC 209668, ATCC 209670, ATCC 209718, ATCC 209784, ATCC 209703, ATCC 209808, ATCC 209810, ATCC 209699, ATCC 209811, ATCC 209813, ATCC 209705, ATCC 209806, ATCC 209809, ATCC 209805, ATCC 209812, ATCC 209844, ATCC 209847, ATCC 209845, ATCC 209843, ATCC 209846, ATCC 209750, ATCC 209848, ATCC 209851, ATCC 209754, ATCC 209747, ATCC 209861, ATCC 209862, ATCC 209867, ATCC 209879, ATCC 209868, ATCC 209869, ATCC 209775, ATCC 209772, ATCC 209774, ATCC 209777, ATCC 209905, ATCC 209855, ATCC 209910, ATCC 209424, ATCC 209720, ATCC 209714, ATCC 209785, ATCC 209911, ATCC 209669, ATCC 209704, ATCC 209702, ATCC 209701, ATCC 209700, ATCC 209814, ATCC 209715, ATCC 209807, ATCC 209753, ATCC 209749, ATCC 209748, ATCC 209842, ATCC 209849, ATCC 209880, ATCC 209864, ATCC 209882, ATCC 209883, ATCC 209865, ATCC 209866, ATCC 209857, ATCC 209870, ATCC 209859, ATCC 209653, ATCC 209389, ATCC 209386, ATCC 203242, ATCC 203243, ATCC 209783, ATCC 209487 or ATCC 209680.

5. A vector comprising the nucleic acid of Claim 1.

6. The vector of Claim 5 operably linked to control sequences recognized by a host cell transformed with the vector.

7. A host cell comprising the vector of Claim 5.

8. The host cell of Claim 7 wherein said cell is a CHO cell.

9. The host cell of Claim 7 wherein said cell is an *E. coli*.

10. The host cell of Claim 7 wherein said cell is a yeast cell.

11. A process for producing a PRO polypeptides comprising culturing the host cell of Claim 7 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.

12. Isolated native sequence PRO polypeptide having at least 80% sequence identity to an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132), Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150), Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270), Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375), Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523) and Figure 225 (SEQ ID NO:526).

13. Isolated PRO polypeptide having at least 80% sequence identity to the amino acid sequence encoded by the nucleotide deposited under accession number ATCC 209791, ATCC 209786, ATCC 209788, ATCC 209787, ATCC 209789, ATCC 209617, ATCC 209620, ATCC 209616, ATCC 209679, ATCC 209654,

ATCC 209655, ATCC 209656, ATCC 209721, ATCC 209717, ATCC 209716, ATCC 209722, ATCC 209668, ATCC 209670, ATCC 209718, ATCC 209784, ATCC 209703, ATCC 209808, ATCC 209810, ATCC 209699, ATCC 209811, ATCC 209813, ATCC 209705, ATCC 209806, ATCC 209809, ATCC 209805, ATCC 209812, ATCC 209844, ATCC 209847, ATCC 209845, ATCC 209843, ATCC 209846, ATCC 209750, ATCC 209848, ATCC 209851, ATCC 209754, ATCC 209747, ATCC 209861, ATCC 209862, ATCC 209867, ATCC 209879, ATCC 209868, ATCC 209869, ATCC 209775, ATCC 209772, ATCC 209774, ATCC 209777, ATCC 209905, ATCC 209855, ATCC 209910, ATCC 209424, ATCC 209720, ATCC 209714, ATCC 209785, ATCC 209911, ATCC 209669, ATCC 209704, ATCC 209702, ATCC 209701, ATCC 209700, ATCC 209814, ATCC 209715, ATCC 209807, ATCC 209753, ATCC 209749, ATCC 209748, ATCC 209842, ATCC 209849, ATCC 209880, ATCC 209864, ATCC 209882, ATCC 209883, ATCC 209865, ATCC 209866, ATCC 209857, ATCC 209870, ATCC 209859, ATCC 209653, ATCC 209389, ATCC 209386, ATCC 203242, ATCC 203243, ATCC 209783, ATCC 209487 or ATCC 209680.

14. A chimeric molecule comprising a polypeptide according to Claim 12 fused to a heterologous amino acid sequence.

15. The chimeric molecule of Claim 14 wherein said heterologous amino acid sequence is an epitope tag sequence.

16. The chimeric molecule of Claim 14 wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

17. An antibody which specifically binds to a PRO polypeptide according to Claim 12.

18. The antibody of Claim 17 wherein said antibody is a monoclonal antibody.

19. An isolated nucleic acid molecule which has at least 80% sequence identity to a nucleic acid which comprises a nucleotide sequence selected from the group consisting of that shown in Figure 5 (SEQ ID NO:8), Figure 6 (SEQ ID NO:9), Figure 7 (SEQ ID NO:10), Figure 12 (SEQ ID NO:29), Figure 13 (SEQ ID NO:30), Figure 16 (SEQ ID NO:37), Figure 17 (SEQ ID NO:38), Figure 18 (SEQ ID NO:39), Figure 31 (SEQ ID NO:75), Figure 64 (SEQ ID NO:170), Figure 71 (SEQ ID NO:191), Figure 96 (SEQ ID NO:265), Figure 99 (SEQ ID NO:271), Figure 100 (SEQ ID NO:272), Figure 101 (SEQ ID NO:273), Figure 102 (SEQ ID NO:274), Figure 103 (SEQ ID NO:275), Figure 104 (SEQ ID NO:276), Figure 105 (SEQ ID NO:277), Figure 106 (SEQ ID NO:278), Figure 107 (SEQ ID NO:279), Figure 110 (SEQ ID NO:285), Figure 111 (SEQ ID NO:286), Figure 112 (SEQ ID NO:287), Figure 113 (SEQ ID NO:288), Figure 114 (SEQ ID NO:289), Figure 115 (SEQ ID NO:290), Figure 116 (SEQ ID NO:291), Figure 123 (SEQ ID NO:304), Figure 126 (SEQ ID NO:310), Figure 127 (SEQ ID NO:311), Figure 130 (SEQ ID NO:323), Figure 133 (SEQ ID NO:331), Figure

134 (SEQ ID NO:332), Figure 137 (SEQ ID NO:338), Figure 140 (SEQ ID NO:347), Figure 143 (SEQ ID NO:353), Figure 174 (SEQ ID NO:431), Figure 175 (SEQ ID NO:432), Figure 188 (SEQ ID NO:457), Figure 205 (SEQ ID NO:484), Figure 220 (SEQ ID NO:516), Figure 223 (SEQ ID NO:524), Figure 226 (SEQ ID NO:527), Figure 227 (SEQ ID NO:528) and Figure 228 (SEQ ID NO:529).

FIGURE 1

CCAGGTCCAACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGGAGGCACAGGTGGCCCCCACCACCCGGAGG
AGCAGCTCCTGCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA
AGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT
TCTGGTGTTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTTAGGGTGTGTGCT
GTCCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCGTGCAGCGTGTGTACCAGCCCTTCC
TCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATTTATAGGACCGCCTAC
CGCCGCAGCCCTGGGCTGGCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAG
GACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAG
GGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG
TCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGC
CGGCAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG
TGCCCAAGGGAGGGCCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAG
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCT
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC
TCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCCTTC
CTGGAGGAGCAGCTGGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGG
CTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGGTC
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTTTTCCTCCTC
CCCTTCCCTCGGGAGGGTCCCCAGACCCTGGCATGGGATGGGCTGGGATTTTTTTGTGAAT
CCACCCCTGGCTACCCCCACCCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA
GCTGAGGGAAGGTACGAGTTCCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC
CGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAA
CGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCT
AGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGT
TACAAAT

FIGURE 2

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGDPV
SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC
GAAICQPPCRNGGSCVQPGRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCW
EGHSLSADGTLCVPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLAS
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

FIGURE 3

CGCTCGCCCCGTCGCCCCTCGCCTCCCCGCAGAGTCCCCTCGCGGCAGCAGATGTGTGTGGG
GTCAGCCCACGGCGGGGACTATGGTGAAATTCCCGGCGCTCACGCACTACTGGCCCCTGATC
CGGTTCTTGGTGCCCCTGGGCATCACCAACATAGCCATCGACTTCGGGGAGCAGGCCTTGAA
CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT
ACTCCCTCATGAAGTTCTTCACGGGTCCCATGAGTGACTTCAAAAATGTGGCCTGGTGTTT
GTGAACAGCAAGAGAGACAGGACCAAAGCCGTCCTGTGTATGGTGGTGGCAGGGGCCATCGC
TGCCGTCTTTCACACACTGATAGCTTATAGTGATTTAGGATACTACATTATCAATAAACTGC
ACCATGTGGACGAGTCGGTGGGGAGCAAGACGAGAAGGGCCTTCCTGTACCTCGCCGCCTTT
CCTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAAACACAAATACAGTTT
CCTGGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTTGTAGCCATTTTGC
TTCACAGTCACCTGGAATGCCGGGAGCCCCTGCTCATCCCGATCCTCTCCTTGTACATGGGC
GCACTTGTGCGCTGCACCACCCTGTGCCTGGGCTACTACAAGAACATTCACGACATCATCCC
TGACAGAAGTGGCCCGGAGCTGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT
GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTCACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTCG
ACAAGAATAACCCCAGCAACAAACTGGTGAGCACGAGCAACACAGTCACGGCAGCCCACATC
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC
ACCCAACGTGTCTGAGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC
TCTGTGTTGTTCCTTTGCGGATCTTCTCCTTCTTCCCAGTTCCAGTCACAGTGAGGGCGCAT
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTCCTTGCCCCCAGCTCTGTGCTGCG
GATCATCGTCCTCATCGCCAGCCTCGTGGTCCTACCCTACCTGGGGGTGCACGGTGCGACCC
TGGGCGTGGGCTCCCTCCTGGCGGGCTTTGTGGGAGAATCCACCATGGTCGCCATCGCTGCG
TGCTATGTCTACCGGAAGCAGAAAAAGAAGATGGAGAATGAGTCGGCCACGGAGGGGGAAGA
CTCTGCCATGACAGACATGCCTCCGACAGAGGAGGTGACAGACATCGTGGAAATGAGAGAGG
AGAATGAATAAGGCACGGGACGCCATGGGCACTGCAGGGACGGTCAGTCAGGATGACACTTC
GGCATCATCTCTTCCCTCTCCCATCGTATTTTGTTCCCTTTTTTTTGTTTTGTTTTGGTAAT
GAAAGAGGCCTTGATTTAAAGGTTTCGTGTCAATTCTCTAGCATACTGGGTATGCTCACACT
GACGGGGGGACCTAGTGAATGGTCTTTACTGTTGCTATGTAAAAACAAACGAAACAACTGAC
TTCATACCCCTGCCTCACGAAAACCCAAAAGACACAGCTGCCTCACGGTTGACGTTGTGTCC
TCCTCCCCTGGACAATCTCCTCTTGGAACCAAAGGACTGCAGCTGTGCCATCGCGCCTCGGT
CACCCTGCACAGCAGGCCACAGACTCTCCTGTCCCCCTTCATCGCTCTTAAGAATCAACAGG
TTAAAACTCGGCTTCCTTTGATTTGCTTCCCAGTCACATGGCCGTACAAAGAGATGGAGCCC
CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGCAG
GAGGCGGGTGGCACGCTGCAGCCCGGAGTCCCCGTTCACACTGAGGAACGGAGACCTGTGAC
CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAAATGCCCCGGG
GGCAGCAAACTGACATGGTTGAATGATAGCATTTCACTCTGCGTTCTCCTAGATCTGAGCAA
GCTGTCAGTTCTCACCCCCACCGTGTATATACATGAGCTAACTTTTTTAAATTGTCACAAAA
GCGCATCTCCAGATTCCAGACCCTGCCGCATGACTTTTCCTGAAGGCTTGCTTTTCCCTCGC
CTTTCCTGAAGGTCGCATTAGAGCGAGTCACATGGAGCATCCTAACTTTGCATTTTAGTTTT
TACAGTGAACTGAAGCTTTAAGTCTCATCCAGCATTCTAATGCCAGGTTGCTGTAGGGTAAC
TTTTGAAGTAGATATATTACCTGGTTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTAA
TTGAGAATGTACTACGGTACTTCCCTCCCACACCATACGATAAAGCAAGACATTTTATAACG
ATACCAGAGTCACTATGTGGTCCTCCCTGAAATAACGCATTCGAAATCCATGCAGTGCAGTA
TATTTTTCTAAGTTTTGGAAAGCAGGTTTTTTCCTTTAAAAAAATTATAGACACGGTTCACT
AAATTGATTTAGTCAGAATTCCTAGACTGAAAGAACCTAAACAAAAAAATATTTTAAAGATA
TAAATATATGCTGTATATGTTATGTAATTTATTTTAGGCTATAATACATTTCCTATTTTCGC
ATTTTCAATAAAATGTCTCTAATACAAAAAA

FIGURE 4

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF
TGPMSDFKNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYIINKLHHVDESV
GSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC
REPLLIPILSLYMGALVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL
ATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN
KLVSTSNTVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLR
IFSFFPVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYLGVHGATLGVGSLL
AGFVGESTMVAIAACYVYRKQKKKMENESATEGEDSAMTDMPPTEEVTDIVEMREENE

FIGURE 5

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTCACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTCG
ACAAGAATAACCCCAGCAACAAACTGGTGAGCACGAGCAACACAGTCACGGCGGCCCACATC
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC
ACCCAACGTGTCTGNGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC
TCTGTGTTGTTCCTTTGCGGATCTTCTCCTTCTTCCCAGTTCCAGTCACAGTGAGGGCGCAT
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTC

FIGURE 6

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG
GAGCAGGGCAAAACAGTNACGGGCAGCCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTTGAT
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTCCTTTGCGGATTTTCT
CCTTTTTCCCAGTTCCAGTCACAGNGAGGGCGCATCTCACCGGGNGGNTGATGACANTGAAG
AAAACCTTTGTCCTTGCCCCCAGCTNTTTGGTGCGGATCATTGTCCTNATNGCCAGCCTTGT
GGTCCTACCCTACCTGGGGGTGCACGGTGCGACCCTGGGCGTGGGTTCCCTCCTGGCGGGCA

FIGURE 7

TATTCCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGACACTGAAGAAA
ACCTTNGTCCTTGCCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT
CCTACCCTACCTGGGGGTGCACGGTGAGAC

FIGURE 8

GCCCCGCGCCCGGCGCCGGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGA
GCCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG
CTGCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCCTCTTCC
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG
CCCTGGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGG
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCT
TCTTTTTCACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG
AATGGGTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGCCTCACCGTGGGTGCCTTCTACAT
CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCCTCTTCA
TCCTCATCCAGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC
AAGGCCGAGGAGTGCGATTCCCGTGCCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTCTT
CTACTTGCTGTCGATCGCGGCCGTGGCGCTGATGTTCATGTACTACACTGAGCCCAGCGGCT
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT
GCTGTCCTGCCCAAGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTCAT
CACCCTCTACACCATGTTTGTCACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA
ACCCCCATTTGCCAACCCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG
ACCCAGTGGTGGGATGCCCCGAGCATTGTGGCCTCATCATCTTCCTCCTGTGCACCCTCTT
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCC
TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCT
GGCCTCACTGCACGTCATGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA
TGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC
TACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTGAGGCAGCCT
CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCT
GCCCCCTCCCCACACCAATCAGCCAGGCTGAGCCCCCACCCCTGCCCCAGCTCCAGGACCTG
CCCCTGAGCCGGGCCTTCTAGTCGTAGTGCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA
GAGCCCCATCCCCCCGCCACACCCACACGGTGGAGCTGCCTCTTCCTTCCCCTCCTCCCTGT
TGCCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCCTCAGGCTCCACGGGAGCGGGG
CTGCTGGAGAGAGCGGGGAACTCCCACCACAGTGGGGCATCCGGCACTGAAGCCCTGGTGTT
CCTGGTCACGTCCCCCAGGGGACCCTGCCCCCTTCCTGGACTTCGTGCCTTACTGAGTCTCT
AAGACTTTTTCTAATAAACAAGCCAGTGCGTGTAAAAAAAA

FIGURE 9

MGACLGACSLLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVE
SQLYKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFTLLMLCVSSSRD
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSW
NQRWLGKAEECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFC
VCVSIAAVLPKVQDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVA
ACEGRAFDNEQDGVTYSYSFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVWVKICAS
WAGLLLYLWTLVAPLLLRNRDFS

FIGURE 10

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTCGAGCCCTCTGGCAGAGGGTTAACCTGGGTC
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGA
AGTCCTGAGCGCTCAAGTTTGTCCGTAGGTCGAGAGAAGGCC<u>ATG</u>GAGGTGCCGCCACCGGC
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCCCGAGTCTTTGCTGCCGAAGCTG
TGACTGCCGATTCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCC
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG
TGTATGGGGGAATACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT
CATTCGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTTTGTGACTATATTCAACACAG
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAATTGCAGGA
GCTGTCACGGGAAGTCTTTTTAGGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCAT
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTG
GTGAGACTGTTCAGGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACTGGAA
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAACC
CTTCAGTAATAGATAAACAAGACAAGGAC<u>TGA</u>AAGTGCTCTGAACTTGAAACTCACTGGAGA
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGTCTTTTTCTTTTCTT
TTTAACTAAGAATGGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT
TATGTTTGTATTAATCTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA
GCAGTAAATAAAACATTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

FIGURE 11

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32190, pI: 9.03, NX(S/T): 2
MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAEIYHNRFDAVQSAH
RAATRGFIRYGWRWGWRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGSLFRINVGLR
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

Important Features:

Signal Peptide:

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and amino acids 171-195

N-glycosylation site:

amino acids 153-156

FIGURE 12

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTCGTTCATG
GCTGGCGCCGAACC

FIGURE 13

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT
TTTTCTGTAGAGCATTGTGCCTATTTCCCCGAGTTTTTGCTGCCGAAGCTGTGACTGCCGAT
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA
ATACCAGCTTTTATTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA
TAACC

FIGURE 14

GAGCCGCCGCCGCGCGCGCGCCGCGCACTGCAGCCCCAGGCCCCGGCCCCCCACCCACGTCT
GCGTTGCTGCCCCGCCTGGGCCAGGCCCCAAAGGCAAGGACAAAGCAGCTGTCAGGGAACCT
CCGCCGGAGTCGAATTTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATGGTTTGCGGGG
GCTTCGCGTGTTCCAAGAACTGCCTGTGCGCCCTCAACCTGCTTTACACCTTGGTTAGTCTG
CTGCTAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT
CGGCGTGGTCATTGCAGTGGGCATCTTCTTGTTCCTGATTGCTTTAGTGGGTCTGATTGGAG
CTGTAAAACATCATCAGGTGTTGCTATTTTTTTATATGATTATTCTGTTACTTGTATTTATT
GTTCAGTTTTCTGTATCTTGCGCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCT
GGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCT
GTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTCTGGCTAGCTGTGTTAAAAGTGACCAC
TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTTGG
TGGCATTGGCCTGTTCTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATACA
GGAACCAGAAAGACCCCCGCGCGAATCCTAGTGCATTCCTTTGATGAGAAAACAAGGAAGAT
TTCCTTTCGTATTATGATCTTGTTCACTTTCTGTAATTTTCTGTTAAGCTCCATTTGCCAGT
TTAAGGAAGGAAACACTATCTGGAAAAGTACCTTATTGATAGTGGAATTATATATTTTTACT
CTATGTTTCTCTACATGTTTTTTTCTTTCCGTTGCTGAAAAATATTTGAAACTTGTGGTCTC
TGAAGCTCGGTGGCACCTGGAATTTACTGTATTCATTGTCGGGCACTGTCCACTGTGGCCTT
TCTTAGCATTTTTACCTGCAGAAAAACTTTGTATGGTACCACTGTGTTGGTTATATGGTGAA
TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCTAC
TGGAAAAAGAGTGGAAATTTATTAAAATCAGAAAGTATGAGATCCTGTTATGTTAAGGGAAA
TCCAAATTCCCAATTTTTTTTGGTCTTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTTAGTA
TAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAAATAGTTAT
GTCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTGGTTT
CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCATCAGAATGGAACGAGTTT
TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAATTTGAAGTCTAA
AAGACTGCATTTTTAAACAAGTTAGTATTAATGCGTTGGCCCACGTAGCAAAAAGATATTTG
ATTATCTTAAAAATTGTTAAATACCGTTTTCATGAAATTTCTCAGTATTGTAACAGCAACTT
GTCAAACCTAAGCATATTTGAATATGATCTCCCATAATTTGAAATTGAAATCGTATTGTGTG
GCTCTGTATATTCTGTTAAAAAATTAAAGGACAGAAACCTTTCTTTGTGTATGCATGTTTGA
ATTAAAAGAAAGTAATGGAAG

FIGURE 15

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVVIAVGIFLFLIALV
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACLALNQEQQGQLLEVGWNNTASARNDIQR
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRFVGGIGLFFSFTEILGVWL
TYRYRNQKDPRANPSAFL

Signal Peptide:
amino acids 1-34

Transmembrane domains:
amino acids 47-63, 72-95 and 162-182

FIGURE 16

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTATATGATTATTCTGTAANT
TGTATTTATTGTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTNTGGCTAGCTGTGTTAA
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC
TACAGATACAGGAACCAG

FIGURE 17

AATCCCAAATTCCCCAATTTTTTTGGNCTTTTTAGGGAAAGATGTGTTGTGGTAAAAAGTGT
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG
TTATGTCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG
TCTAAAAGACTGCATTTTTAAACAAGTTAGTATTAATGCGTTGGCCCACGTAGCAAAAAGAT
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTCATGAAAGTTCTCAGTATTGTAACAGC
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCCATAATTTGAAATTGAAATCGTATT
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC
CCACTTGC

FIGURE 18

ATGATTATTCTGTTACTTGTATTTATTGTTCAGTTTTATGGTATCTTGCGCTTGTTTAGCCC
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG
TGACTCCGCAAATGACATCCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTTAACCC
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA
TCATAGGAGAATATGC

FIGURE 19

CAGTCACCATGAAGCTGGGCTGTGTCCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG
CTCTGGGTGGCCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGT
CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT
TCCAGGTCAAGGCCTACACTTTCAGTGAACCCTTCCACCTGATTGTGTCCTATGACTGGCTG
ATCCTCCAAGGTCCAGCCAAGCCAGTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC
CCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC
TGCAGTGGCATCTTCCAGAGCCCTGGTCCTGGGATCCCAGAAACAGCATCTGTTGTGGCTAT
CACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG
CAGGAAGCCCCATGACCCTGAGTTGTCAGACAAAGTTGCCCCTGCAGAGGTCAGCTGCCCGC
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCATACTGGTGTGAGGCAGCCACTGAGG
ACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT
GCTGCACCTCCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAACTGCTCCTGA
GGAGGCCCCTGGGCCTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG
CAGGATGTGAGAGTCCTCCTCGGTCACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAGTAAACAGTTCATCCATGATCTCACT
TAACCACCCCAATAAATCTGATTCTTTATTTTCTCTTCCTGTCCTGCACATATGCATAAGTA
CTTTTACAAGTTGTCCCAGTGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAAATAAATTT
ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAA
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCCAGAGGACA
TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGGTTGGGGGATGGTGGGATGT
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG
GGCAGTACCCCACAACGAAAAATAATCTGGCCCAAAATGTCAGTTGTACTGAGTTTGAGAAA
CCCCAGCCTAATGAAACCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT
TATCTCTTTCCAGCCTCATTCAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGCTATG
GTCTGTTCTTTAGTTCTAGTTTGTATCCCCTCAAAAGCCATTATGTTGAAATCCTAATCCCC
AAGGTGATGGCATTAAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC
ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCCTTCCACCAT
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTCGCCAAACACCG
ACTCTGTCGTTGCCTTGATCTTGAACTTCCAGCCTCCAGAACTATGAGAAATAAAATTCTGG
TTGTTTGTAGCCTAA

FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594
><subunit 1 of 1, 359 aa, 1 stop
><MW: 38899, pI: 5.21, NX(S/T): 0

MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCQAWQDWPLTQVTFYRDGSALGPPGP
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS
PMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ
VWKQSPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPPTPSSEDPGFSSPL
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Leucine zipper pattern sequence:
amino acids 12-33

Protein kinase C phosphorylation site:
amino acids 353-355

FIGURE 21

CCCACGCGTCCGCCCACGCGTCCGCCCACGGGTCCGCCCACGCGTCCGGGCCACCAGAAGTT
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTG<u>ATG</u>GGG
ATCTTACTGGGCCTGCTACTCCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT
GGAAGTGCCAGAGAGTGTAACAGGACCTTGGAAAGGGGATGTGAATCTTCCCTGCACCTATG
ACCCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCT
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAGGGCCG
CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCCTGGAGATGG
ATGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCCTGATGGCAACCAAGTCGTG
AGAGATAAGATTACTGAGCTCCGTGTCCAGAAACTCTCTGTCTCCAAGCCCACAGTGACAAC
TGGCAGCGGTTATGGCTTCACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC
GGGGTTCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACCAGGAACCCATC
AAAGTAGCAACCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA
TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC
TTGAAAGCAACATCTACAGTGAAGCAGTCCTGGGACTGGACCACTGACATGGATGGCTACCT
TGGAGAGACCAGTGCTGGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT
CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTCGGAAGACATCCCAA
CAAGAGCATGTCTACGAAGCAGCCAGG<u>TAA</u>GAAAGTCTCTCCTCTTCCATTTTTGACCCCGT
CCCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAGACCC
AATCCTAAGGCCGGAGGCCTTCAGGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC
AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT
CCAGTGATGAGCCAACTTCCCAGAATCTGGGCAACAACTACTCTGATGAGCCCTGCATAGGA
CAGGAGTACCAGATCATCGCCCAGATCAATGGCAACTACGCCCGCCTGCTGGACACAGTTCC
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTTAAAAATGCCCCATTAGGC
CAGGATCTGCTGACATAATTGCCTAGTCAGTCCTTGCCTTCTGCATGGCCTTCTTCCCTGCT
ACCTCTCTTCCTGGATAGCCCAAAGTGTCCGCCTACCAACACTGGAGCCGCTGGGAGTCACT
GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTTGGCTCTGG
GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG
CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA
CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT
TTCTCTTTCTTCAGGGCCAGACAGCTTTTAATTGAAATTGTTATTTCACAGGCCAGGGTTCA
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA
ATCATAACAGC

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416
><subunit 1 of 1, 321 aa, 1 stop
><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQRGS
DPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQ
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQQTNNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMT
YPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFTMAYIMLCRKT
SQQEHVYEAAR

Glycosaminoglycan attachment site:
amino acids 149-152

Transmembrane domain:
amino acids 276-306

FIGURE 23

GCGCCGGGAGCCCATCTGCCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACAT
GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCCAGCTCGCCCGAGGTCCGTCGGA
GGCGCCCGGCCGCCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC
GGG<u>ATG</u>TCCCTCCTCCTTCTCCTCTTGCTAGTTTCCTACTATGTTGGAACCTTGGGGACTCA
CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA
GTGGTGATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
AGTGGCCTTTGCTTCCAATTTCCTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGC
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT
GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTGTGTATT
ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT
GACTACAACCACCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA
CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACTGTACAGT
ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG
ATTTTCCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT
CCTCTTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCCTCCACTCGCTCCACAGCAAAT
AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCCAGCCAGGGCTGGCCAC
CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG
CTAATCTGACCAAAGCAGAAACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA
ACGGTC<u>TGA</u>ATTACAATGGACTTGACTCCCACGCTTTCCTAGGAGTCAGGGTCTTTGGACTC
TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA
GTGAGCATTGCACGGAACAGATTCAGATGAGCATTTTCCTTATACAATACCAAACAAGCAAA
AGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG
AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG
AGGTGAATATACCTAAAACTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTCACAATT
TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTTCTATGCATTTCTGCAAACTTATTGGATT
ATTAGTTATTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC
TGAGCTAACCACTTCTAAGAAACTCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
TTCATTTGTCATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAAC
TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCCCTCAAAT
CAGATGCCTCTAAGGACTTTCCTGCTAGATATTTCTGGAAGGAGAAAATACAACATGTCATT
TATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA
CCCAACATACCATTATAGTCTCTTCTTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Transmembrane domain:
amino acids 221-254

FIGURE 25

GTCGTTCCTTTGCTCTCTCGCGCCCAGTCCTCCTCCCTGGTTCTCCTCAGCCGCTGTCGGAG
GAGAGCACCCGGAGACGCGGGCTGCAGTCGCGGCGGCTTCTCCCCGCCTGGGCGGCCTCGCC
GCTGGGCAGGTGCTGAGCGCCCCTAGAGCCTCCCTTGCCGCCTCCCTCCTCTGCCCGGCCGC
AGCAGTGCACATGGGGTGTTGGAGGTAGATGGGCTCCCGGCCCGGGAGGCGGCGGTGGATGC
GGCGCTGGGCAGAAGCAGCCGCCGATTCCAGCTGCCCCGCGCGCCCCGGGCGCCCCTGCGAG
TCCCCGGTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCCTGCAGCCGC
ATCGCCCGCCGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCCTGCTTGGATTCCTTAG
CACCACCACAGCTCAGCCAGAACAGAAGGCCTCGAATCTCATTGGCACATACCGCCATGTTG
ACCGTGCCACCGGCCAGGTGCTAACCTGTGACAAGTGTCCAGCAGGAACCTATGTCTCTGAG
CATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCTGTGGGGACCTTTACCAGGCA
TGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAATGATTGAGA
AATTACCTTGTGCTGCCTTGACTGACCGAGAATGCACTTGCCCACCTGGCATGTTCCAGTCT
AACGCTACCTGTGCCCCCCATACGGTGTGTCCTGTGGGTTGGGGTGTGCGGAAGAAAGGGAC
AGAGACTGAGGATGTGCGGTGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCTTCTA
GTGTGATGAAATGCAAAGCATACACAGACTGTCTGAGTCAGAACCTGGTGGTGATCAAGCCG
GGGACCAAGGAGACAGACAACGTCTGTGGCACACTCCCGTCCTTCTCCAGCTCCACCTCACC
TTCCCCTGGCACAGCCATCTTTCCACGCCCTGAGCACATGGAAACCCATGAAGTCCCTTCCT
CCACTTATGTTCCCAAAGGCATGAACTCAACAGAATCCAACTCTTCTGCCTCTGTTAGACCA
AAGGTACTGAGTAGCATCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGGAA
GGAAGACGTGAACAAGACCCTCCCAAACCTTCAGGTAGTCAACCACCAGCAAGGCCCCCACC
ACAGACACATCCTGAAGCTGCTGCCGTCCATGGAGGCCACTGGGGGCGAGAAGTCCAGCACG
CCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAGCATTTTGACATCAA
TGAGCATTTGCCCTGGATGATTGTGCTTTTCCTGCTGCTGGTGCTTGTGGTGATTGTGGTGT
GCAGTATCCGGAAAAGCTCGAGGACTCTGAAAAAGGGGCCCCGGCAGGATCCCAGTGCCATT
GTGGAAAAGGCAGGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTA
CTACTGCAATGGCCATGGTATCGATATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGT
GGAAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAGAGGGAGGTTGCTGCTTTCTCCAAT
GGGTACACAGCCGACCACGAGCGGGCCTACGCAGCTCTGCAGCACTGGACCATCCGGGGCCC
CGAGGCCAGCCTCGCCCAGCTAATTAGCGCCCTGCGCCAGCACCGGAGAAACGATGTTGTGG
AGAAGATTCGTGGGCTGATGGAAGACACCACCCAGCTGGAAACTGACAAACTAGCTCTCCCG
ATGAGCCCCAGCCCGCTTAGCCCGAGCCCCATCCCCAGCCCCAACGCGAAACTTGAGAATTC
CGCTCTCCTGACGGTGGAGCCTTCCCCACAGGACAAGAACAAGGGCTTCTTCGTGGATGAGT
CGGAGCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCCTCCGCGCTGAGCAGGAACGGT
TCCTTTATTACCAAAGAAAAGAAGGACACAGTGTTGCGGCAGGTACGCCTGGACCCCTGTGA
CTTGCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGATTG
AAGAGATTCCCCAGGCTGAGGACAAACTAGACCGGCTATTCGAAATTATTGGAGTCAAGAGC
CAGGAAGCCAGCCAGACCCTCCTGGACTCTGTTTATAGCCATCTTCCTGACCTGCTGTAGAA
CATAGGGATACTGCATTCTGGAAATTACTCAATTTAGTGGCAGGGTGGTTTTTTAATTTTCT
TCTGTTTCTGATTTTTGTTGTTTGGGGTGTGTGTGTGTGTTTGTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGTGTTTAACAGAGAATATGGCCAGTGCTTGAGTTCTTTCTCCTTCTCTCTCT
CTCTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTATAAGCCTTTGCCAGGTGTAACT
GTTGTGAAATACCCACCACTAAAGTTTTTTAAGTTCCATATTTTCTCCATTTTGCCTTCTTA
TGTATTTTCAAGATTATTCTGTGCACTTTAAATTTACTTAACTTACCATAAATGCAGTGTGA
CTTTTCCCACACACTGGATTGTGAGGCTCTTAACTTCTTAAAAGTATAATGGCATCTTGTGA
ATCCTATAAGCAGTCTTTATGTCTCTTAACATTCACACCTACTTTTTAAAAACAAATATTAT
TACTATTTTTATTATTGTTTGTCCTTTATAAATTTTCTTAAAGATTAAGAAAATTTAAGACC
CCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTT
CATATTCATGGCTGAAACTTGACCACACTATTGCTGATTGTATGGTTTTCACCTGGACACCG
TGTAGAATGCTTGATTACTTGTACTCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAA
ATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTTGACAACTGGGCCACCAAAGAACTTG
AACTTCACCTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACTTTGGAAAGTCAAAA
TCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCCAGCTTTGCTTTAAAAGATGTCTT
GTTTTTTATATACACATAATCAATAGGTCCAATCTGCTCTCAAGGCCTTGGTCCTGGTGGGA
TTCCTTCACCAATTACTTTAATTAAAAATGGCTGCAACTGTAAGAACCCTTGTCTGATATAT
TTGCAACTATGCTCCCATTTACAAATGTACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCA
AAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTTTGTGGGTAGTGGTGAAGGACCGATATC
AGAAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTTGTTAAAAAAAAAA

FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594
><subunit 1 of 1, 655 aa, 1 stop
><MW: 71845, pI: 8.22, NX(S/T): 8

MGTSPSSSTALASCSRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIGTYRHVDRATG
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMIEKLPCA
ALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRKKGTETEDVRCKQCARGTFSDVPSSVMKC
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHIL
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIVVCSIRK
SSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNREKWIYYCNGHGIDILKLVAAQVGSQWKDIY
QFLCNASEREVAAFSNGYTADHERAYAALQHWTIRGPEASLAQLISALRQHRRNDVVEKIRG
LMEDTTQLETDKLALPMSPSPLSPSPIPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLL
RCDSTSSGSSALSRNGSFITKEKKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ
AEDKLDRLFEIIGVKSQEASQTLLDSVYSHLPDLL

FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTGGGA
CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCAC
CATGGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTGGCC
TTGATGATTTGAAAATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG
TCACTGCTGCCATTGAAGTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC
GAGTACCGCTGTGTCCGGGTGGGTGGTCAGAATGCCGTGCTCCAGGTGTTCACAGCTGCTTC
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCCAAC
TGGGTTTCCCAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGCAGTTC
CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA
CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCAGTGCACAGCCT
GTGGTCATAGAAGGGGCTACAGCTCACGCATCGTGGGTGGAAACATGTCCTTGCTCTCGCAG
TGGCCCTGGCAGGCCAGCCTTCAGTTCCAGGGCTACCACCTGTGCGGGGGCTCTGTCATCAC
GCCCCTGTGGATCATCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGA
CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG
ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT
GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCCTGCCCAACTCTGAAGAGA
ACTTCCCCGATGGAAAAGTGTGCTGGACGTCAGGATGGGGGGCCACAGAGGATGGAGGTGAC
GCCTCCCCTGTCCTGAACCACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCACAG
GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG
TGGACAGCTGCCAGGGGGACAGCGGGGGGCCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG
TTAGTGGGAGCGACCAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC
CCGTGTCACCTCCTTCCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAA
GAGGAAGGGGACAAGTAGCCACCTGAGTTCCTGAGGTGATGAAGACAGCCCGATCCTCCCCT
GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCCTTGGAGCTCTGAGTTCCGGCACCA
GTAGCAGGCCCGAAAGAGGCACCCTTCCATCTGATTCCAGCACAACCTTCAAGCTGCTTTTT
GTTTTTTGTTTTTTTGAGGTGGAGTCTCGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGAAA
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCCTCAGCTTCCCCA
GTAGCTGGGACCACAGGTGCCCGCCACCACACCCAACTAATTTTTGTATTTTTAGTAGAGAC
AGGGTTTCACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT
CAGCCTCCCACAGTGCTGGGATTACAGGCATGGGCCACCACGCCTAGCCTCACGCTCCTTTC
TGATCTTCACTAAGAACAAAAGAAGCAGCAACTTGCAAGGGCGGCCTTTCCCACTGGTCCAT
CTGGTTTTCTCTCCAGGGTCTTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCACG
TGCAAAGCCACCAACAGCCACTCAGAAAAGACGCACCAGCCCAGAAGTGCAGAACTGCAGTC
ACTGCACGTTTTCATCTCTAGGGACCAGAACCAAACCCACCCTTTCTACTTCCAAGACTTAT
TTTCACATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAGGCCTATTTTCATGATTTCTT
TGTAGCATTTGGTGCTTGACGTATTATTGTCCTTTGATTCCAAATAATATGTTTCCTTCCCT
CATTGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAATCAAAATCATCCACTGAAA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234
><subunit 1 of 1, 453 aa, 1 stop
><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAAS
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHH
SVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT
PLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHR
DVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYT
RVTSFLDWIHEQMERDLKT

FIGURE 29

CCCACGCGTCCGTCCTAGTCCCCGGGCCAACTCGGACAGTTTGCTCATTTATTGCAACGGTC
AAGGCTGGCTTGTGCCAGAACGGCGCGCGCGCGCACGCACGCACACACACGGGGGAAAC
TTTTTTAAAAATGAAAGGCTAGAAGAGCTCAGCGGCGGCGCGGGCGCTGCGCGAGGGCTCCG
GAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTCGCGACGCCCGGCCCCGGCTCGGCGCCC
GCGTGGGATGGTGCAGCGCTCGCCGCCGGGCCCGAGAGCTGCTGCACTGAAGGCCGGCGACG
ATGGCAGCGCGCCCGCTGCCCGTGTCCCCCGCCCGCGCCCTCCTGCTCGCCCTGGCCGGTGC
TCTGCTCGCGCCCTGCGAGGCCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAG
TTGTCAGTGCCTCTGTTCGGAGTGGGACCTCTGGATCCCAGTGAAGAGCTTCGACTCCAAG
AATCATCCAGAAGTGCTGAATATTCGACTACAACGGGAAAGCAAAGAACTGATCATAAATCT
GGAAAGAAATGAAGGTCTCATTGCCAGCAGTTTCACGGAAACCCACTATCTGCAAGACGGTA
CTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGTACGGGGA
TATTCTGATTCAGCAGTCAGTCTCAGCACGTGTTCTGGTCTCAGGGGACTTATTGTGTTTGA
AAATGAAAGCTATGTCTTAGAACCAATGAAAAGTGCAACCAACAGATACAAACTCTTCCCAG
CGAAGAAGCTGAAAAGCGTCCGGGGATCATGTGGATCACATCACAACACACCAAACCTCGCT
GCAAAGAATGTGTTTCCACCACCCTCTCAGACATGGGCAAGAAGGCATAAAAGAGAGACCCT
CAAGGCAACTAAGTATGTGGAGCTGGTGATCGTGGCAGACAACCGAGAGTTTCAGAGGCAAG
GAAAAGATCTGGAAAAAGTTAAGCAGCGATTAATAGAGATTGCTAATCACGTTGACAAGTTT
TACAGACCACTGAACATTCGGATCGTGTTGGTAGGCGTGGAAGTGTGGAATGACATGGACAA
ATGCTCTGTAAGTCAGGACCCATTCACCAGCCTCCATGAATTTCTGGACTGGAGGAAGATGA
AGCTTCTACCTCGCAAATCCCATGACAATGCGCAGCTTGTCAGTGGGGTTTATTTCCAAGGG
ACCACCATCGGCATGGCCCCAATCATGAGCATGTGCACGGCAGACCAGTCTGGGGGAATTGT
CATGGACCATTCAGACAATCCCCTTGGTGCAGCCGTGACCCTGGCACATGAGCTGGGCCACA
ATTTCGGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAAA
GGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAG
CAGGAAGGACTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTTAACCTGCCGG
AAGTCAGGGAGTCTTTCGGGGGCCAGAAGTGTGGGAACAGATTTGTGGAAGAAGGAGAGGAG
TGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTGCTGCAATGCCACCACCTGTACCCT
GAAGCCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCTGAAGCCTGCAG
GAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCCAGAGTTCTGCACAGGGGCCAGC
CCTCACTGCCCAGCCAATGTGTACCTGCACGATGGGCACTCATGTCAGGATGTGGACGGCTA
CTGCTACAATGGCATCTGCCAGACTCACGAGCAGCAGTGTGTCACGCTCTGGGGACCAGGTG
CTAAACCTGCCCCTGGGATCTGCTTTGAGAGAGTCAATTCTGCAGGTGATCCTTATGGCAAC
TGTGGCAAAGTCTCGAAGAGTTCCTTTGCCAAATGCGAGATGAGAGATGCTAAATGTGGAAA
AATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGGTACCAATGCCGTTTCCATAGAAA
CAAACATCCCTCTGCAGCAAGGAGGCCGGATTCTGTGCCGGGGGACCCACGTGTACTTGGGC
GATGACATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTG
CCTGAATCGTCAATGTCAAAATATTAGTGTCTTTGGGGTTCACGAGTGTGCAATGCAGTGCC
ACGGCAGAGGGGTGTGCAACAACAGGAAGAACTGCCACTGCGAGGCCCACTGGGCACCTCCC
TTCTGTGACAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCCCCATCCGGCAAGCAGAAGC
AAGGCAGGAAGCTGCAGAGTCCAACAGGGAGCGCGGCCAGGGCCAGGAGCCCGTGGGATCGC
AGGAGCATGCGTCTACTGCCTCACTGACACTCATCTGAGCCCTCCCATGACATGGAGACCGT
GACCAGTGCTGCTGCAGAGGAGGTCACGCGTCCCCAAGGCCTCCTGTGACTGGCAGCATTGA
CTCTGTGGCTTTGCCATCGTTTCCATGACAACAGACACAACACAGTTCTCGGGGCTCAGGAG
GGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAACAGTGCAAGGAAGGGCAGCGACTTCCTG
GTTGAGCTTCTGCTAAAACATGGACATGCTTCAGTGCTGCTCCTGAGAGAGTAGCAGGTTAC
CACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTCAC
TGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCCAGTGTCCCCTTTCCCCAGTGA
CACCTCAGCCTTGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGC
TTTTAGCATTTATTATATGAAAATAGCAGGGTTTTAGTTTTTAATTTATCAGAGACCCTGCC
ACCCATTCCATCTCCATCCAAGCAAACTGAATGGCAATGAAACAAACTGGAGAAGAAGGTAG
GAGAAAGGGCGGTGAACTCTGGCTCTTTGCTGTGGACATGCGTGACCAGCAGTACTCAGGTT
TGAGGGTTTGCAGAAAGCCAGGGAACCCACAGAGTCACCAACCCTTCATTTAACAAGTAAGA
ATGTTAAAAAGTGAAAACAATGTAAGAGCCTAACTCCATCCCCCGTGGCCATTACTGCATAA
AATAGAGTGCATTTGAAAT

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624
><subunit 1 of 1, 735 aa, 1 stop
><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVSASVRSGDLWIPVKSFDSK
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCYYHGHVRG
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLA
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGKDLEKVKQRLIEIANHVDKF
YRPLNIRIVLVGVEVWNDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFGMNHDTLDRGCSCQMAVEK
GGCIMNASTGYPFPMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEE
CDCGEPEECMNRCCNATTCTLKPDAVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS
PHCPANVYLHDGHSCQDVDGYCYNGICQTHEQQCVTLWGPGAKPAPGICFERVNSAGDPYGN
CGKVSKSSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIETNIPLQQGGRILCRGTHVYLG
DDMPDPGLVLAGTKCADGKICLNRQCQNISVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP
FCDKFGFGGSTDSGPIRQAEARQEAAESNRERGQGQEPVGSQEHASTASLTLI

FIGURE 31

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA
ACAAAACAGTTTTGGGGGTTCAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA
AGAGGACTCAAAAGTTTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT
GGGCCCAGTGTCCCCTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT
AGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

FIGURE 32

CATCCTGCAACATGGTGAAACCACGCCTGGCTAATTTTGTTGTATTTTTGGTAGAGATGGGA
TTTCACCGTGTTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCGCCTCGGCCTCCC
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGGCCACAAACTTTTTAAGAAGTTAAT
GAAACCATACCTTTTACATTTTTAATGACAGGAAAATGCTCACAATAATTGTTAACCCAAAA
TTCTGGATACAAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAATA
TACCAAATATCAATAATACTTATCTCTGGGTAAAAACCTCTTCTCATACCCTGTGCTAACAA
CTTTTAACAAAAAAATTTGCATCACTTTTAAGAATCAAGAAAAATTTCTGAAGGTCATATGGG
ACAGAAAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAAGATTCGAAATCTGCCT
TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTTCTAAGCAACTTAAATGTTTTGTTTCGA
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGGAGTGATGTCACTGCCATTATGATGCCCC
TTGAATATAAGACCCTACTTGCTATCTCCCCTGCACCAGCCAGGAGCCACCCATCCTCCAGC
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAAATGGGTAAGGGGATGGTGGCGA
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTTCTTCATTTGTT
CCTTTAACCAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCAACAGTGCCCT
ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAGAGG
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAAACCGAATCCAAATGGTGCCT
AGAAGTTCAATGTGGCAAGGAAAAAAACCAGGTCTTCATCAAATCTACTAATTTCACTCCTT
ATTAACAGAGAAACGCTTGAGAGTCTCAAACTGGACTGGTTTAAAGAGCATCTGAAGGATTT
GACTAGATGATAAATGCCTGTACTCCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG
AGGTCAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA
AATATTGACTGGGCGTGGTGGTGAGTGCCTGTGATCCCAGCTACTCAGGTGGCTGAAGCAGG
ACAATCACTTGAACTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAAAGCCAAGTGCAGTGGCT
CACGCCTGTAATCCCGGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGGAGATCA
AGACCATCCTGGCTAATACAGTGAAACCCTGTCTCTACTAAAAATACAAAAAATTAGCCGGG
GATGGTGGCAGGCACCTGGAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATAGCGTGAA
CTCAGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309
><subunit 1 of 1, 67 aa, 1 stop
><MW: 6981, pI: 7.47, NX(S/T): 0
MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVVLLAL
LHLYH

FIGURE 34

GCCGCGGCGAGAGCGCGCCCAGCCCCGCCGCG<u>ATG</u>CCCGCGCGCCCAGGACGCCTCCTCCCG
CTGCTGGCCCGGCCGGCGGCCCTGACTGCGCTGCTGCTGCTGCTGGGCCATGGCGGCGG
CGGGCGCTGGGGCGCCCGGGCCCAGGAGGCGGCGGCGGCGGCGGACGGGCCCCCGCGG
CAGACGGCGAGGACGGACAGGACCCGCACAGCAAGCACCTGTACACGGCCGACATGTTCACG
CACGGGATCCAGAGCGCCGCGCACTTCGTCATGTTCTTCGCGCCCTGGTGTGGACACTGCCA
GCGGCTGCAGCCGACTTGGAATGACCTGGGAGACAAATACAACAGCATGGAAGATGCCAAAG
TCTATGTGGCTAAAGTGGACTGCACGGCCCACTCCGACGTGTGCTCCGCCCAGGGGGTGCGA
GGATACCCCACCTTAAAGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGGTCCTCG
GGACTTCCAGACACTGGAAAACTGGATGCTGCAGACACTGAACGAGGAGCCAGTGACACCAG
AGCCGGAAGTGGAACCGCCCAGTGCCCCCGAGCTCAAGCAAGGGCTGTATGAGCTCTCAGCA
AGCAACTTTGAGCTGCACGTTGCACAAGGCGACCACTTTATCAAGTTCTTCGCTCCGTGGTG
TGGTCACTGCAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCTTGAACATTCCG
AAACTGTCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACTCTGCTCCGGAAACCAG
GTTCGTGGCTATCCCACTCTTCTCTGGTTCCGAGATGGGAAAAAGGTGGATCAGTACAAGGG
AAAGCGGGATTTGGAGTCACTGAGGGAGTACGTGGAGTCGCAGCTGCAGCGCACAGAGACTG
GAGCGACGGAGACCGTCACGCCCTCAGAGGCCCCGGTGCTGGCAGCTGAGCCCGAGGCTGAC
AAGGGCACTGTGTTGGCACTCACTGAAAATAACTTCGATGACACCATTGCAGAAGGAATAAC
CTTCATCAAGTTTTATGCTCCATGGTGTGGTCATTGTAAGACTCTGGCTCCTACTTGGGAGG
AACTCTCTAAAAAGGAATTCCCTGGTCTGGCGGGGGTCAAGATCGCCGAAGTAGACTGCACT
GCTGAACGGAATATCTGCAGCAAGTATTCGGTACGAGGCTACCCCACGTTATTGCTTTTCCG
AGGAGGGAAGAAAGTCAGTGAGCACAGTGGAGGCAGAGACCTTGACTCGTTACACCGCTTTG
TCCTGAGCCAAGCGAAAGACGAACTT<u>TAG</u>GAACACAGTTGGAGGTCACCTCTCCTGCCCAGC
TCCCGCACCCTGCGTTTAGGAGTTCAGTCCCACAGAGGCCACTGGGTTCCCAGTGGTGGCTG
TTCAGAAAGCAGAACATACTAAGCGTGAGGTATCTTCTTTGTGTGTGTGTTTTCCAAGCCAA
CACACTCTACAGATTCTTTATTAAGTTAAGTTTCTCTAAGTAAATGTGTAACTCATGGTCAC
TGTGTAAACATTTTCAGTGGCGATATATCCCCTTTGACCTTCTCTTGATGAAATTTACATGG
TTTCCTTTGAGACTAAAATAGCGTTGAGGGAAATGAAATTGCTGGACTATTTGTGGCTCCTG
AGTTGAGTGATTTTGGTGAAAGAAAGCACATCCAAAGCATAGTTTACCTGCCCACGAGTTCT
GGAAAGGTGGCCTTGTGGCAGTATTGACGTTCCTCTGATCTTAAGGTCACAGTTGACTCAAT
ACTGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAAACCCACACCTCTGGAAGATAC
CTTCACGGCCGCTGCTGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGC
CGTGATGAAAGCAGCGTTACTTCTGACCGTGCCTGAGTAAGAGAATGCTGATGCCATAACTT
TATGTGTCGATACTTGTCAAATCAGTTACTGTTCAGGGGATCCTTCTGTTTCTCACGGGGTG
AAACATGTCTTTAGTTCCTCATGTTAACACGAAGCCAGAGCCCACATGAACTGTTGGATGTC
TTCCTTAGAAAGGGTAGGCATGGAAAATTCCACGAGGCTCATTCTCAGTATCTCATTAACTC
ATTGAAAGATTCCAGTTGTATTTGTCACCTGGGGTGACAAGACCAGACAGGCTTTCCCAGGC
CTGGGTATCCAGGGAGGCTCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTC
TGATTCTGTTTCTCAGTAGTCCTTTTAGAGGCTTGCTATACTTGGTCTGCTTCAAGGAGGTC
GACCTTCTAATGTATGAAGAATGGGATGCATTTGATCTCAAGACCAAAGACAGATGTCAGTG
GGCTGCTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCCTCTAACTCA
TGCTGTCCTTGTGATTAAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAGCT
CTAAGATAGATAGGTGTTTGTCCTTTTACCATCGAGCTACTTCCCATAATAACCACTTTGCA
TCCAACACTCTTCACCCACCTCCCATACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACT
GGTGGTAGGAATCTTAGAAACAAGACCACTTATACTGTCTGTCTGAGGCAGAAGATAACAGC
AGCATCTCGACCAGCCTCTGCCTTAAAGGAAATCTTTATTAATCACGTATGGTTCACAGATA
ATTCTTTTTTTAAAAAAACCCAACCTCCTAGAGAAGCACAACTGTCAAGAGTCTTGTACACA
CAACTTCAGCTTTGCATCACGAGTCTTGTATTCCAAGAAAATCAAAGTGGTACAATTTGTTT
GTTTACACTATGATACTTTCTAAATAAACTCTTTTTTTTTAA

FIGURE 35

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47629, pI: 5.90, NX(S/T): 0
MPARPGRLLPLLARPAALTALLLLLLGHGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS
KHLYTADMFTHGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAH
SDVCSAQGVRGYPTLKLFKPGQEAVKYQGPRDFQTLENWMLQTLNEEPVTPEPEVEPPSAPE
LKQGLYELSASNFELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT
QHYELCSGNQVRGYPTLLWFRDGKKVDQYKGKRDLESLREYVESQLQRTETGATETVTPSEA
PVLAAEPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL

FIGURE 36

CTTTTCTGAGGAACCACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA
CCGCTGAAGTCTGTGCCACACACACAATTTCACCAGGACCCAAAGGAGATGATGGTGAAAAA
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTGGGAAGA
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACTGGATATTAGTATTGCTCGGCT
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAAT
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGG
GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC
CAAGAGTGGCTTCTTTCGGGTGTTCATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA
TGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT
ACGTATTTGCTATTTTCCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTCCTG
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT
CCATCATCAAAAAAAAAAAAAAAA

FIGURE 37

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDPGEEG
KHGKVGRMGPKGIKGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKGKAGTVCDCGRY
RKFVGQLDISIARLKTSMKFVKNVIAGIRETEEKFYYIVQEEKNYRESLTHCRIRGGMLAMP
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC
VEMLSSGRWNDTECHLTMYFVCEFIKKKK

FIGURE 38

GGTTCTATCGATTCGAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCTGCTCTCCGCCCGTGTGGAGTGGTGGGGCCTGGGTGGAATGGGCGTGT
GCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTT
CGGAAGGGAGGATCAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGC
GGGCTCCATGGCTGCCCTCCTGCTGCTGCCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA
AGCTACACCTCTGGCCGCAGTTGCGCTGGCTTCCGGCGGACTTGGCCTTTGCGGTGCGAGCT
CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCGACCCGGAAGG
TCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACTGGCCCAGCAGCGCGCCGCGC
ACACCTTTCTCATTCACGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC
AGGGCTGCACGCGCCTTCCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCGGCGACAG
CGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGGAGCCGGAGATGCAGCGGCCG
GAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAGGTGGAGGAGCCGCCGCCCCT
CTGTCACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCCAGAGTTTCTGTGGCTCTG
GTTCGGGCTGGCCAAGGCCGGCCTGCGCACTGCCTTTGTGCCCACCGCCCTGCGCCGGGGCC
CCCTGCTGCACTGCCTCCGCAGCTGCGGCGCGCGCGCTGGTGCTGGCGCCAGAGTTTCTG
GAGTCCCTGGAGCCGGACCTGCCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGG
CCCAGGAACCCACCCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG
GGCCAGTGCCAGGATACCTCTCTTCCCCCAGAGCATAACAGACACGTGCCTGTACATCTTC
ACCTCTGGCACCACGGGCCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG
CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCCAC
TCTACCACATGTCCGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTG
GTGCTGAAATCCAAGTTCTCGGCTGGTCAGTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC
GGTGTTCCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACCAGCCCCCGAGCAAGGCAG
AACGTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCCAGATACCTGGGAGCGT
TTTGTGCGGCGCTTCGGGCCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT
GGCCACCATCAACTACACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCCTGGCTTTACAAGC
ATATCTTCCCCTTCTCCTTGATTCGCTATGATGTCACCACAGGAGAGCCAATTCGGGACCCC
CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCA
GCAGTCCCCATTCCTGGGCTATGCTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGG
ATGTCTTCCGGCCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC
CACAACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATG
GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCCC
CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCACCTTATGCCCG
GCCCCGATTCCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG
TTCGGATGGCAAATGAGGGCTTCGACCCCAGCACCCTGTCTGACCCACTGTACGTTCTGGAC
CAGGCTGTAGGTGCCTACCTGCCCCTCACAACTGCCCGGTACAGCGCCCTCCTGGCAGGAAA
CCTTCGAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGGG
CCGTTGCAGGTGTACTGGGCTGTCAGGGATCTTTTCTATACCAGAACTGCGGTCACTATTTT
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTCTGACCTAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC
TTGGCCGCCATGGCCCAACTTGTTTATTGCAG

FIGURE 39

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913
><subunit 1 of 1, 730 aa, 1 stop
><MW: 78644, pI: 7.65, NX(S/T): 2

MGVCQRTRAPWKEKSQLERAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLPL
LLLKLHLWPQLRWLPADLAFAVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ
RAAHTFLIHGSRRFSYSEAERESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERAAPGAGD
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGLAKAGLRTAFVPTAL
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA
EVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP
SKAERGHKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW
LYKHIFPFSLIRYDVTTGEPIRDPQGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPELAQGK
LLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEV
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPPYARPRFLRLQESLATTETFK
QQKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARYSALLAGNLRI

Signal peptide:
aa 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation site
starting at aa 136

CUB domain protein motif
aa 254-261

putative AMP-binding domain siganture
aa 332-343

N-glycosylation sites
aa 37-40 and 483-486

FIGURE 40

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA
CACATCCCCAAGAACCTCGAGCTCACACCAACAGACACACGCGCGCATACACACTCGCTCTC
GCTTGTCCATCTCCCTCCCGGGGGAGCCGGCGCGCGCTCCCACCTTTGCCGCACACTCCGGC
GAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGAACTCGGATTGCAGCTCTGAACCC
CCATGGTGGTTTTTTAAACACTTCTTTTCCTTCTCTTCCTCGTTTTGATTGCACCGTTTCCA
TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCCAGCCAGCCCTTGTTGGCTTGCCATCGT
CCATCTGGCTTATAAAAGTTTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCTCGG
CTGGCAGAAGGGGGTGACGCTGGGCAGCGGCGAGGAGCGCGCCGCTGCCTCTGGCGGGCTTT
CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCCGTGGGGTTTACCGAGCTGGATTTGTATG
TTGCACCATGCCTTCTTGGATCGGGGCTGTGATTCTTCCCCTCTTGGGGCTGCTGCTCTCCC
TCCCCGCCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCCAGGCGTACGGTGCC
AAGGGATTCAGCCTGGCGGACATCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG
TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAAC
TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGG
CATAAGAAATTTGACGAATTTTTCCGAGAGCTCCTGGAGAATGCAGAAAAGTCACTAAATGA
TATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTCAGAAGTCTTCCAGGACCTCT
TCACAGAGCTGAAAAGGTACTACACTGGGGGTAATGTGAATCTGGAGGAAATGCTCAATGAC
TTTTGGGCTCGGCTCCTGGAACGGATGTTTCAGCTGATAAACCCTCAGTATCACTTCAGTGA
AGACTACCTGGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCC
GGAAACTGAAGATTCAGGTTACCCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG
ACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAAGGTCAGCCCAACCCCAGGGTGTATCCG
TGCCCTCATGAAGATGCTGTACTGCCCATACTGTCGGGGGCTTCCCACTGTGAGGCCCTGCA
ACAACTACTGTCTCAACGTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG
TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACAT
TGAGTCGGTCATGGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA
ACAGCATGCAGGTGTCTGCAAAGGTCTTTCAGGGATGTGGTCAGCCCAAACCTGCTCCAGCC
CTCAGATCTGCCCGCTCAGCTCCTGAAAATTTTAATACACGTTTCAGGCCCTACAATCCTGA
GGAAAGACCAACAACTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA
AATTGAAGCTCTCTAAAAAGGTCTGGTCAGCATTACCCTACACTATCTGCAAGGACGAGAGC
GTGACAGCGGGCACGTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT
GCCTGAGATCATGAATGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACA
TCACTCGGCCTGACACTTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA
CTAAAAAACGCCTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG
CTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCCCACGGAGTTTGAGTTTGTCACCA
CAGAGGCCCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCCAGCGTGGC
CACTCCCTGCTCTCCTGGTCTCTCACCTGCATTGTCCTGGCACTGCAGAGACTGTGCAGATA
ATCTTGGGTTTTTGGTCAGATGAAACTGCATTTTAGCTATCTGAATGGCCAACTCACTTCTT
TTCTTACACTCTTGGACAATGGACCATGCCACAAAAACTTACCGTTTTCTATGAGAAGAGAG
CAGTAATGCAATCTGCCTCCCTTTTTGTTTTCCCAAAGAGTACCGGGTGCCAGACTGAACTG
CTTCCTCTTTCCTTCAGCTATCTGTGGGGACCTTGTTTATTCTAGAGAGAATTCTTACTCAA
ATTTTTCGTACCAGGAGATTTTCTTACCTTCATTTGCTTTTATGCTGCAGAAGTAAAGGAAT
CTCACGTTGTGAGGGTTTTTTTTTCTCATTTAAAT

FIGURE 41

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914
><subunit 1 of 1, 555 aa, 1 stop
><MW: 62736, pI: 5.36, NX(S/T): 0
MPSWIGAVILPLLGLLLSLPAGADVKARSCGEVRQAYGAKGFSLADIPYQEIAGEHLRICPQ
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKSLNDMF
VRTYGMLYMQNSEVFQDLFTELKRYYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFSEDY
LECVSKYTDQLKPFGDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAERLEGPFNIES
VMDPIDVKISEAIMNMQENSMQVSAKVFQGCGQPKPAPALRSARSAPENFNTRFRPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGHSKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMDDVCPTEFEFVTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCT
GAGAAAACGCACGCAGTTTGCAGCGCCTGCGCCGGGTGCGCCAACTACGCAAAGACCAAGCG
GGCTCCGCGCGGACCGGCCGCGGGGCTAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAG
CGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGTGGAGGGAGATCAGGAAACGGCTT
CTTCCTCACTTCGCCGCCTGGTGAGTGTCGGGGAGATTGGCAAACGCCTAGGAAAGGACTGG
GGAAAATAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGGTCCACTACGGCAGTTTAT
CTGTCTGATCAGAGCCAGACGCGACGCGTCCACTTCGCAGTTCTTTCCAGGTGTGGGACCG
CAGGACAGACGGCCGATCCCGCCGCCCTCCGTACCAGCACTCCCAGGAGAGTCAGCCTCGCT
CCCCAACGTCGAGGGCGCTCTGGCCACGAAAAGTTCCTGTCCACTGTGATTCTCAATTCCTT
GCTTGGTTTTTTTCTCCAGAGAACTTTTGGGTGGAGATATTAACTTTTTTCTTTTTTTTTTT
CCTTGGTGGAAGCTGCTCTAGGGAGGGGGGAGGAGGAGGAGAAAGTGAAATGTGCTGGAGAA
GAGCGAGCCCTCCTTGTTCTTCCGGAGTCCCATCCATTAAGCCATCACTTCTGGAAGATTAA
AGTTGTCGGACATGGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTC
ACCGTCTGTTGGGTGCATGTGTGCGCCCGCAGCGGCGCGGGGCGCGTGGTTCTCCGCGTGGA
GTCTCACCTGGGACCTGAGTGAATGGCTCCCAGGGGCTGTGCGGGGCATCCGCCTCCGCCTT
CTCCACAGGCCTGTGTCTGTCCTGGAAAGATGCTAGCAATGGGGGCGCTGGCAGGATTCTGG
ATCCTCTGCCTCCTCACTTATGGTTACCTGTCCTGGGGCCAGGCCTTAGAAGAGGAGGAAGA
AGGGGCCTTACTAGCTCAAGCTGGAGAGAAACTAGAGCCCAGCACAACTTCCACCTCCCAGC
CCCATCTCATTTTCATCCTAGCGGATGATCAGGGATTTAGAGATGTGGGTTACCACGGATCT
GAGATTAAAACACCTACTCTTGACAAGCTCGCTGCCGAAGGAGTTAAACTGGAGAACTACTA
TGTCCAGCCTATTTGCACACCATCCAGGAGTCAGTTTATTACTGGAAAGTATCAGATACACA
CCGGACTTCAACATTCTATCATAAGACCTACCCAACCCAACTGTTTACCTCTGGACAATGCC
ACCCTACCTCAGAAACTGAAGGAGGTTGGATATTCAACGCATATGGTCGGAAAATGGCACTT
GGGTTTTAACAGAAAAGAATGCATGCCCACCAGAAGAGGATTTGATACCTTTTTTGGTTCCC
TTTTGGGAAGTGGGGATTACTATACACACTACAAATGTGACAGTCCTGGGATGTGTGGCTAT
GACTTGTATGAAAACGACAATGCTGCCTGGGACTATGACAATGGCATATACTCCACACAGAT
GTACACTCAGAGAGTACAGCAAATCTTAGCTTCCCATAACCCCACAAAGCCTATATTTTTAT
ATACTGCCTATCAAGCTGTTCATTCACCACTGCAAGCTCCTGGCAGGTATTTCGAACACTAC
CGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTTCCTGCTTAGATGAAGC
AATCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTCTATAACAACAGCATTATCATTT
ACTCTTCAGATAATGGTGGCCAGCCTACGGCAGGAGGGAGTAACTGGCCTCTCAGAGGTAGC
AAAGGAACATATTGGGAAGGAGGGATCCGGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAA
AAACAAGGGAACAGTGTGTAAGGAACTTGTGCACATCACTGACTGGTACCCCACTCTCATTT
CACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCTGGGAGACC
ATAAGTGAGGGTCTTCGCTCACCCCGAGTAGATATTTTGCATAACATTGACCCCTATACACC
AAGGCAAAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGC
CATCAGAGTGCAGCACTGGAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCC
CTCAGTCTTTCAGCAACCTGGGACCGAACCGGTGGCACAATGAACGGATCACCTTGTCAACT
GGCAAAAGTGTATGGCTTTTCAACATCACAGCCGACCCATATGAGAGGGTGGACCTATCTAA
CAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCACAGTTCAACAAAACTGCAG
TGCCGGTCAGGTATCCCCCCAAAGACCCCAGAAGTAACCCTAGGCTCAATGGAGGGGTCTGG
GGACCATGGTATAAAGAGGAAACCAAGAAAAAGAAGCCAAGCAAAAATCAGGCTGAGAAAAA
GCAAAAGAAAAGCAAAAAAAAGAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACCAGCAA
ATTTGGCTCGATAATATCGCTGGCCTAAGCGTCAGGCTTGTTTTCATGCTGTGCCACTCCAG
AGACTTCTGCCACCTGGCCGCCACACTGAAAACTGTCCTGCTCAGTGCCAAGGTGCTACTCT
TGCAAGCCACACTTAGAGAGAGTGGAGATGTTTATTTCTCTCGCTCCTTTAGAAAACGTGGT
GAGTCCTGAGTTCCACTGCTGTGCTTCAGTCAACTGACCAAACACTGCTTTGAATTATAGGA
GGAGAACAATAACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGA
TTAAAACTACCTTTGATAAATTACAGTCAAAGATTGTGTCACCTCAAAGGCCTTGAAGAATA
TATTTTCTTGGTGAATTTTTGTATGTCTGTCATATGACACTTGGGTTTTTTAATTAATTCTA
TTTTATATATATATAAATATATGTTTCTTTTCCTGTGAAAAGCTGTTTTTCTCACATGTGAACA
GCTTGCACCTCATTTTACCATGCGTGAGGGAATGGCAAATAAGAATGTTTGAGCACACTGCC
CACAATGAATGTAACTATTTTCTAAACACTTTACTAGAAGAACATTTCAGTATAAAAAACCT
AATTTATTTTTACAGAAAAATATTTTGTTGTTTTTATAAAAAGTTATGCAAATGACTTTTAT
TTTTATTTCCTGCATACCATTAGAAGAATTTTATTTCATTTCTTCAAATTATCAAGCACTGT
AATACTATAAATTAATGTAATACTGTGTGAATTCAGACTATAAAAAACATCATTCAGAAAAC
TTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATATTCCTTACAA

FIGURE 42B

ATTACTTGGAAATTCAATGTTTGTGCAGAGTTGAGACAACTTTATTGTTTCTATCATAAACT
ATTTATGTATCTTAATTATTAAAATGATTTACTTTATGGCACTAGAAAATTTACTGTGGCTT
TTCTGATCTAACTTCTAGCTAAAATTGTATCATTGGTCCTAAAAAATAAAAATCTTTACTAA
TAGGCAATTGAAGGAATGGTTTGCTAACAACCACAGTAATATAATATGATTTTACAGATAGA
TGCTTCCCCTTGGCTATGACATGGAGAAAGATTTTCCCATAATAATAACTAATATTTATATT
AGGTTGGTGCAAAACTAGTTGCGGTTTTTCCCATTAAAAGTAATAACCTTACTCTTATACAA
AGTGGACACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCCTGGAGTAGGTAAC
CTTGCTTGGAAACCCCACATGCAAACGTCATGAGGAGAATTAAAGGAGTATTATCAGTAATG
AAGTTTATCATGGGTCATCAATGAGCATAGATTGGTGTGGATCCTGTAGACCCTGGTGTTTT
CTTTGAAGTGCCCTCTCCTAATGCAGAGGCCTTGAAGCTTACAGTATACACTTGAAAAGTCA
CAGATAGCTAGAATTATGATCTTTGAAGTTATAACTGTGATCTGAAAATGTGTGTGGTGGTA
TGACAGCATACCATTAAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTTA
TATCACAACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAAT
GTATAAAAGAATCTATAATCTAGTACTGAAATTACTAAATTGGGTAAGATGATTTAAATGAT
TTTAATTTTAACATTTTATTTCTAGAATATATGGCTCCATTTTATTTTATAGTGTAAAGTTG
TATTTCCTAAAGTTTGTGTTTTGTCGACAGTATCTTTTAAATGAGTCTTAAAAATAAAGGCA
TATTGTTCATGTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATAAAGGCA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 43

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296
><subunit 1 of 1, 515 aa, 1 stop
><MW: 56885, pI: 6.49, NX(S/T): 5
MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTYGYLSWGQALEEEEEGALLAQA
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYHGSEIKTPTLDKLAAEGVKLENYYVQPICTP
SRSQFITGKYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVGYSTHMVGKWHLGFNRKEC
MPTRRGFDTFFGSLLGSGDYYTHYKCDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTQRVQQ
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLDEAINNVTLA
LKTYGFYNNSIIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGFVHSPLLKNKGTVCK
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG
QQAMGSGTLQSSQPSECSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFS
TSQPTHMRGWTYLTGIQES

Important Features:

Signal Peptide:
amino acids 1-37

Sulfatases signature 1.
amino acids 120-132

Sulfatases signature 2.
amino acids 168-177

Tyrosine kinase phosphorylation site.
amino acids 163-169

N-glycosylation sites.
amino acids 157-160, 306-309 and 318-321

FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC
CCGTGCGAGA<u>ATG</u>CCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTGCTCTCCTGGGTGGCAG
GTGGTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTTGTTAGCATCGGCACGTCAGCCT
GGGGTCTGTCACTATGGAACTAAACTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAGTGCGTGGGACCAAACAAAT
GCAGATGCTTTCCAGGATACACCGGGAAAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG
AAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCTTTTGCCT
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACTCTAGGACATGTGCCATGATAA
ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA
CTCCGCCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAAATGTCACA
TTGGTTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT
ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCCTTCAAGTG
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTTCTGCTATCCCTGAAAATTCTG
TGAAGGAAGTCCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC
AAAAACAGCATGAAAAAGAAGGCAAAAATTAAAAATGTTACCCCAGAACCCACCAGGACTCC
TACCCCTAAGGTGAACTTGCAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGAACT
CTCATGGAGGTAAAAAAGGGAATGAAGAGAAA<u>TGA</u>AAGAGGGGCTTGAGGATGAGAAAAGAG
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTTCCCT
AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACTTCCAA
ACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACT
GGAAACAGGATAGAGAAGATGATTTTGACTGGAATCCTGCTGATCGAGATAATGCTATTGGC
TTCTATATGGCAGTTCCGGCCTTGGCAGGTCACAAGAAAGACATTGGCCGATTGAAACTTCT
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG
ACAAAGTCGGGAAACTTCGAGTGTTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG
ACCACGAGTGAGGATGAAAAGTGGAAGACAGGGAAAATTCAGTTGTATCAAGGAACTGATGC
TACCAAAAGCATCATTTTTGAAGCAGAACGTGGCAAGGGCAAAACCGGCGAAATCGCAGTGG
ATGGCGTCTTGCTTGTTTCAGGCTTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG
TTACTATCTTTATATTTGACTTTGTATGTCAGTTCCCTGGTTTTTTTGATATTGCATCATAG
GACCTCTGGCATTTTAGAATTACTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATTG
TAAGATGCCTTTCTTGTATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT
TCTCAGTCATTTCTGAATCTTTCCNCATTATATTATAAAATNTGGAAANGTCAGTTTATCTC
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTTCTA
GAAAATAGAAAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGGA
AACTATGACATCAAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC
TTGTATATTTAATTCTTTGTAATAATAA

FIGURE 45

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCE
ATCEPGCKFGECVGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGSYKCFCLSGH
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP
YNRRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPTPK
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

Signal peptide:
amino acids 1-21

EGF-like domain cysteine pattern signature.
amino acids 80-91

Calcium-binding EGF-like domains
amino acids 103-124, 230-251 and 185-206

FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGCTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCC
AGAATGGGAGCTGACTGAT<u>ATG</u>GTGGTGTGGGTGACTGGAGCCTCGAGTGGAATTGGTGAGG
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGTGCTGTCAGCCAGAAGAGTGCAT
GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAAGATATACT
TGTTTTGCCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAATGTCCCAGCGTTCTCTGTGC
ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTC
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA
ATAGCATCCTGGGTATCATATCTGTACCTCTTTCCATTGGATACTGTGCTAGCAAGCATGCT
CTCCGGGGTTTTTTTAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC
TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA
CAAAGACTATAGGCAATAATGGAGACCAGTCCCACAAGATGACAACCAGTCGTTGTGTGCGG
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACAACCTTTCTT
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAAATC
TTTAAGACAAAACA<u>TGA</u>CTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT
ACTTTTTAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAAATAATAAAAG
ATTGCCATGAATCTTGCAAAA

FIGURE 47

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343
><subunit 1 of 1, 289 aa, 1 stop
><MW: 32268, pI: 9.21, NX(S/T): 0
MVVWVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPLDL
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQRSLCMDTSLDVYRKLIELNYLGTVSLTKCVL
PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGP
VQSNIVENSLAGEVTKTIGNNGDQSHKMTTSRCVRLMLISMANDLKEVWISEQPFLLVTYLW
QYMPTWAWWITNKMGKKRIENFKSGVDADSSYFKIFKTKHD

Important Features:
Signal Peptide:
amino acids 1-31

Transmembrane domain:
amino acids 136-157

Tyrosine kinase phosphorylation site.
106-113 and 107-114

Homologous region to Short-chain alcohol dehydrogenase
amino acids 80-90, 131-168, 1-13 and 176-185

FIGURE 48

GCGACGTGGGCACCGCCATCAGCTGTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC
GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTCGG
TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCCTCTGTCC
TG<u>ATG</u>CTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTC
TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT
GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCCAGGGCAAGGCTAAGAGGCACTGAGCCCTCA
ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCCTGTG
GACAGCGTGGCCCCGGCCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC
TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC
CTGGGTCCTCACTGCTGCCCACTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGGT
CAGTGGTCCTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG
GCTGCCCTGCAGTTGCCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT
GCAGCTCGCCCACCCCACGACCCACACACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCC
CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGACC
CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACTGTATCTACAACCAGCT
GCACCAGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGTGGGGGCCCCCAGCCTG
GGGTGCAGGGCCCCTGTCAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGA
CACTGGGTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGT
GCTGCTGACCAACACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTT
TCCTGGCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA
TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCCTCCCCATGGCCCTGGGAGGCCAGGCT
GATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTCAGAGGAGGCGGTGCTAACTG
CTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGA
CCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGG
CTACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC
TCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG
GCCCGCCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAG
GGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG
TGTGTACCAGTGCTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGTCTGGGGCACCACTGGTG
CATGAGGTGAGGGGCACATGGTTCCTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG
CCCCGCCAGGCCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGGGTCAGCAGTTTGG
ACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCGAGGCTGAGCCTGGAAGCTGCCTGGCC
AACATAAGCCAACCAACCAGCTGC<u>TGA</u>CAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC
AGGCAGGCAAATGGCATTACTGCCCCTGTCCTCCCCACCCTGTCATGTGTGATTCCAGGCAC
CAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGGTGCCCA
CTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCCACACCCAACTCTGCTACCAAGC
AGGCGTCTCAGCTTTCCTCCTCCTTTACTCTTTCAGATACAATCACGCCAGCCACGTTGTTT
TGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCCTTTTTTTAAACTTAAATAAATTGTTAC
AAAATAAAA

FIGURE 49

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571
MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV
PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGA
EEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTS
DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLC
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSDEDS
CVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSV
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERG
WVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTSAVGELPSCEGLS
GAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEP
GSCLANISQPTSC

Important features:

Signal peptide:

amino acids 1-15

Homologous region to Serine proteases, trypsin family

amino acids 79-95, 343-359 and 237-247

N-glycosylation sites.

amino acids 37-40 and 564-567

Kringle domains

amino acids 79-96, 343-360 and 235-247

FIGURE 50

CGGGCCGCCCCCGGCCCCCATTCGGGCCGGGCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG
GCCGCGTCCCTGAGTCCCAGAGTCGGCGCGGCGCGGCAGGGGCAGCCTTCCACCACGGGGAG
CCCAGCTGTCAGCCGCCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGT
GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCC
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACA
GCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC
TCTTCCCGGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGCGTGTGGCG
GACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTCGGCAGCGCTGCCGTCAGCCT
GCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTC
TGGCAGGATGGGCAGGGTGTGCCCCTGACTGGCAACGTGACCACGTCGCAGATGGCCAACGA
GCAGGGCTTGTTTGATGTGCACAGCGTCCTGCGGGTGGTGCTGGGTGCGAATGGCACCTACA
GCTGCCTGGTGCGCAACCCCGTGCTGCAGCAGGATGCGCACRGCTCTGTCACCATCACAGGG
CAGCCTATGACATTCCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT
TGCACTGCTGGTGGCCCTGGCTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGG
GAGCTGCTACCCCTCCCTACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC
TGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC
AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTT
TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT
GCCTTATTTCACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCTC
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTCAGA
CTGACTGACCCCCTGCCTTATTTCACCAAAGACACGATGCATAGTCACCCCGGCCTTGTTTC
TCCAATGGCCGTGATACACTAGTGATCATGTTCAGCCCTGCTTCCACCTGCATAGAATCTTT
TCTTCTCAGACAGGGACAGTGCGGCCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCCTTTC
CCCTCCTTCCTCCCTGCCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG
AGGGGACTGCCCCCCACCCCCACCATGGTGCTATTCTGGGGCTGGGGCAGTCTTTTCCTGGC
TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG
GATGTCATCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC
TCGGAGGGATTTTGTAAACTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 51

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386
><subunit 1 of 1, 316 aa, 1 stop, 1 unknown
><MW: -1, pI: 4.62, NX(S/T): 4
MLRRRGSPGMGVHVGAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPEPGFSLAQ
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGVPL
TGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA
LWVTVGLSVCLIALLVALAFVCWRKIKQSCEEENAGAEDQDGEGEGSKTALQPLKHSDSKED
DGQEIA

Important features:
Signal peptide:
amino acids 1-28

Transmembrane domain:
amino acids 251-270

N-glycosylation site.
amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC
amino acids 217-234

FIGURE 52

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC
CTGAACTTGTCTGAAGCCCTTGTCCGTAAGCCTTGAACTACGTTCTTAAATCTATGAAGTCG
AGGGACCTTTCGCTGCTTTTGTAGGGACTTCTTTCCTTGCTTCAGCAAC<u>ATG</u>AGGCTTTTCT
TGTGGAACGCGGTCTTGACTCTGTTCGTCACTTCTTTGATTGGGGCTTTGATCCCTGAACCA
GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTCATCTGCCATCGCAAGACCAAAGGAGGGGA
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC
ACAAACATAACAATGGTCAGCCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT
TGGGACCAGGGCTTGAAAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCCTCCTGC
TCTGGGCTATGGAAAAGAAGGAAAAGGTAAAATTCCCCCAGAAAGTACACTGATATTTAATA
TTGATCTCCTGGAGATTCGAAATGGACCAAGATCCCATGAATCATTCCAAGAAATGGATCTT
AATGATGACTGGAAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA
ACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTGATAAAG
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA
<u>TAG</u>AGATACATCTACCCTTTTAATATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAA
AGAACATTTTATTTTTATACAATGTTCTTTCTTGCTTTGTTTTTATTTTTATATATTTTTT
CTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTTCTGATAAGTTATT
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTTCACTTTCACAG
ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAAATGTTGCAACTGGGAATATACC
ACGACATGAGACCAGGTTATAGCACAAATTAGCACCCTATATTTCTGCTTCCCTCTATTTTC
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT
GTTATAATGAAATAGTTTATGTGTAACTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA
TGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG
TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAG
GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA
CCCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCCTGTAATCCCAGCT
ACCCAGGAAGGCTGAGGCGGCAGAATCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAG
ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAAAAGAACACGGTTAATACCATATNA
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGGCTCCTAGTGAT
TGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC
TAGCGGAATATCCTTCCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA
TTGTATCATAAGATAAAGTAGTAAACCAGTCTACATTTTCCCATTTCTGTCTCATCAAAAAC
TGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGGGCCAAGGAGGG
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTA
CTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGCACACCTGTAGTCCCAGCTACTCGGGAG
GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCC
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAAGAAGCAGA
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

FIGURE 53

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194
><subunit 1 of 1, 211 aa, 1 stop
><MW: 24172, pI: 5.99, NX(S/T): 1
MRLFLWNAVLTLFVTSLIGALIPEPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSL
FHSTHKHNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPEST
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVED
IFDKEDEDKDGFISAREFTYKHDEL

Important features:

Signal peptide:
amino acids 1-20

N-glycosylation site.
amino acids 176-179

Casein kinase II phosphorylation site.
amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.
amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase
amino acids 78-114 and 118-131

EF-hand calcium-binding domain.
amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain
amino acids 183-203

FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTAGCAT
CCAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCCTCTCCCGTAGCCCACCCGA
CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT
CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTAC
CTGCCACCCTCAACGTCCTCAATGGCTCTGACGCCCGCCTGCCCTGCACCTTCAACTCCTGC
TACACAGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACTGCTC
TGAGGAGATGTTCCTCCAGTTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAG
ACCGCGTGGAGTTCTCAGGGAACCCCAGCAAGTACGATGTGTCGGTGATGCTGAGAAACGTG
CAGCCGGAGGATGAGGGGATTTACAACTGCTACATCATGAACCCCCCTGACCGCCACCGTGG
CCATGGCAAGATCCATCTGCAGGTCCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG
CCGTGATTGTGGGTGCCTCCGTCGGGGGCTTCCTGGCTGTGGTCATCTTGGTGCTGATGGTG
GTCAAGTGTGTGAGGAGAAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA
GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCC
CTGCAGCCTCCCGTGTCCCGTCTCCTCCCCTCTCCGCCCTGTACAGTGACCCTGCCTGCTCG
CTCTTGGTGTGCTTCCCGTGACCTAGGACCCCAGGGCCCACCTGGGGCCTCCTGAACCCCCG
ACTTCGTATCTCCCACCCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA
TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGGCTCCCACCTGCCAGTCCCTGG
GGGGAGGCAGGAGGCACATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA
GGAGGGGCCGCTGTCACCTGCCCAGTGCTTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTGG
GGAGGGAGGGCTTTCCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTG
TGCTCCTCCCCTGCTCCCAGCCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCCTGA
AACTTGGAGGGGCATGTTAAAGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGG
CTGCAGGCAAAGCTGGACATGTGCCCTGGCCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT
GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG
ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCCAGCGGGGACCCACCAACAGAGGCC
AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTTGCTGCAG
GCTCTGCCTTCTCCATGGGGTAACCACCCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAAT
GAGGAGGCCATGCACAGGGTGGGGCAGCTTTCTTTGGGGCTTCAGTGAGAACTCTCCCAGTT
GCCCTTGGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAGGGAAAGCCTGAGGCCG
GCATAAGGGGAGGCCTTGGAACCTGAGCTGCCAATGCCAGCCCTGTCCCATCTGCGGCCACG
CTACTCGCTCCTCTCCCAACAACTCCCTTCGTGGGGACAAAAGTGACAATTGTAGGCCAGGC
ACAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGGATTACCTCCAT
CTGTTTAGTAGAAATGGGCAAAACCCCATCTCTACTAAAAATACAAGAATTAGCTGGGCGTG
GTGGCGTGTGCCTGTAATCCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG
GGAAGCAGAGGTTGCAGTGAACTGAGATAGTGATAGTGCCACTGCAATTCAGCCTGGGTGAC
ATAGAGAGACTCCATCTCAAAAAAAA

FIGURE 55

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415
<subunit 1 of 1, 215 aa, 1 stop
<MW: 24326, pI: 6.32, NX(S/T): 4
MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMLRNVQPEDEGI
YNCYIMNPPDRHRGHGKIHLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

Important features:
Signal peptide:
amino acids 1-20

Transmembrane domain:
amino acids 161-179

Immunoglobulin-like fold:
amino acids 83-127

N-glycosylation sites.
amino acids 42-45, 66-69 and 74-77

FIGURE 56

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC
TCAATGGCTCTGACGCCCGCCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC
AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACTGCTCTGAGGAGATGTTCCTCCAG
TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG
GAACCCCAGCAAGTACGATGTGTCGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA
TTTACAACTGCTACATCATGAACCCCCC

FIGURE 57

TCACGGGGCTCATCTCTTTTTCTCTTTGGTGCCCACCAGGACGGAGCATGGAGGTNCACATA
CCTGCCACCCTCAACGTCCTCAATGGCTTTGACGCCCGCCTGCCCTGCACCTTCAACTCCNG
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACTGGC
TCTGAGGAGATGTTCCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCCAGCAAGTACGATGTGTCGGTGATGC
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAACTGCTACATCATGAACCCCCC

FIGURE 58

TGCGGCGACCGTCGTACACCATGGGCCTCCACCTCCGCCCCTACCGTGTGGGGCTGCTCCCG
GATGGCCTCCTGTTCCTCTTGCTGCTGCTAATGCTGCTCGCGGACCCAGCGCTCCCGGCCGG
ACGTCACCCCCCAGTGGTGCTGGTCCCTGGTGATTTGGGTAACCAACTGGAAGCCAAGCTGG
ACAAGCCGACAGTGGTGCACTACCTCTGCTCCAAGAAGACCGAAAGCTACTTCACAATCTGG
CTGAACCTGGAACTGCTGCTGCCTGTCATCATTGACTGCTGGATTGACAATATCAGGCTGGT
TTACAACAAAACATCCAGGGCCACCCAGTTTCCTGATGGTGTGGATGTACGTGTCCCTGGCT
TTGGGAAGACCTTCTCACTGGAGTTCCTGGACCCCAGCAAAAGCAGCGTGGGTTCCTATTTC
CACACCATGGTGGAGAGCCTTGTGGGCTGGGGCTACACACGGGGTGAGGATGTCCGAGGGGC
TCCCTATGACTGGCGCCGAGCCCCAAATGAAAACGGGCCCTACTTCCTGGCCCTCCGCGAGA
TGATCGAGGAGATGTACCAGCTGTATGGGGGCCCCGTGGTGCTGGTTGCCCACAGTATGGGC
AACATGTACACGCTCTACTTTCTGCAGCGGCAGCCGCAGGCCTGGAAGGACAAGTATATCCG
GGCCTTCGTGTCACTGGGTGCGCCCTGGGGGGGCGTGGCCAAGACCCTGCGCGTCCTGGCTT
CAGGAGACAACAACCGGATCCCAGTCATCGGGCCCCTGAAGATCCGGGAGCAGCAGCGGTCA
GCTGTCTCCACCAGCTGGCTGCTGCCCTACAACTACACATGGTCACCTGAGAAGGTGTTCGT
GCAGACACCCACAATCAACTACACACTGCGGGACTACCGCAAGTTCTTCCAGGACATCGGCT
TTGAAGATGGCTGGCTCATGCGGCAGGACACAGAAGGGCTGGTGGAAGCCACGATGCCACCT
GGCGTGCAGCTGCACTGCCTCTATGGTACTGGCGTCCCCACACCAGACTCCTTCTACTATGA
GAGCTTCCCTGACCGTGACCCTAAAATCTGCTTTGGTGACGGCGATGGTACTGTGAACTTGA
AGAGTGCCCTGCAGTGCCAGGCCTGGCAGAGCCGCCAGGAGCACCAAGTGTTGCTGCAGGAG
CTGCCAGGCAGCGAGCACATCGAGATGCTGGCCAACGCCACCACCCTGGCCTATCTGAAACG
TGTGCTCCTTGGGCCCTGACTCCTGTGCCACAGGACTCCTGTGGCTCGGCCGTGGACCTGCT
GTTGGCCTCTGGGGCTGTCATGGCCCACGCGTTTTGCAAAGTTTGTGACTCACCATTCAAGG
CCCCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGCTGTTTGTTATCCTTTCTCTG
TGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAATGCT
GCTGATGGTGGAACTGCTGTGACCTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGCCCTG
GTCCCAGTCCCTGCCTGGGGCCATGTGTCCCCCTATTCCTGTGGGCTTTTCATACTTGCCTA
CTGGGCCCTGGCCCCGCAGCCTTCCTATGAGGGATGTTACTGGGCTGTGGTCCTGTACCCAG
AGGTCCCAGGGATCGGCTCCTGGCCCCTCGGGTGACCCTTCCCACACACCAGCCACAGATAG
GCCTGCCACTGGTCATGGGTAGCTAGAGCTGCTGGCTTCCCTGTGGCTTAGCTGGTGGCCAG
CCTGACTGGCTTCCTGGGCGAGCCTAGTAGCTCCTGCAGGCAGGGGCAGTTTGTTGCGTTCT
TCGTGGTTCCCAGGCCCTGGGACATCTCACTCCACTCCTACCTCCCTTACCACCAGGAGCAT
TCAAGCTCTGGATTGGGCAGCAGATGTGCCCCCAGTCCCGCAGGCTGTGTTCCAGGGGCCCT
GATTTCCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGCCTCCCTTCACCCTGGGACTGT
GGTTCCAAGGATGAGAGCAGGGGTTGGAGCCATGGCCTTCTGGGAACCTATGGAGAAAGGGA
ATCCAAGGAAGCAGCCAAGGCTGCTCGCAGCTTCCCTGAGCTGCACCTCTTGCTAACCCCAC
CATCACACTGCCACCCTGCCCTAGGGTCTCACTAGTACCAAGTGGGTCAGCACAGGGCTGAG
GATGGGGCTCCTATCCACCCTGGCCAGCACCCAGCTTAGTGCTGGGACTAGCCCAGAAACTT
GAATGGGACCCTGAGAGAGCCAGGGGTCCCCTGAGGCCCCCCTAGGGGCTTTCTGTCTGCCC
CAGGGTGCTCCATGGATCTCCCTGTGGCAGCAGGCATGGAGAGTCAGGGCTGCCTTCATGGC
AGTAGGCTCTAAGTGGGTGACTGGCCACAGGCCGAGAAAAGGGTACAGCCTCTAGGTGGGGT
TCCCAAAGACGCCTTCAGGCTGGACTGAGCTGCTCTCCCACAGGGTTTCTGTGCAGCTGGAT
TTTCTCTGTTGCATACATGCCTGGCATCTGTCTCCCCTTGTTCCTGAGTGGCCCCACATGGG
GCTCTGAGCAGGCTGTATCTGGATTCTGGCAATAAAAGTACTCTGGATGCTGTAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 59

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189
><subunit 1 of 1, 412 aa, 1 stop
><MW: 46658, pI: 6.65, NX(S/T): 4
MGLHLRPYRVGLLPDGLLFLLLLLMLLADPALPAGRHPPVVLVPGDLGNQLEAKLDKPTVVH
YLCSKKTESYFTIWLNLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDVRVPGFGKTFSL
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEEMYQ
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI
PVIGPLKIREQQRSAVSTSWLLPYNYTWSPEKVFVQTPTINYTLRDYRKFFQDIGFEDGWLM
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLLGP

Important features:

Signal peptide:
amino acids 1-28

Potential lipid substrate binding site:
amino acids 147-164

N-glycosylation sites.
amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins
amino acids 189-201

Beta-transducin family Trp-Asp repeat
amino acids 353-365

FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGG
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTG
AGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGT
GGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAAC
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCAT
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAA
CGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAA
GGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCA
GCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC
TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCT
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGA
CCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT
CAGCTTCCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG
ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCA
CTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGT
GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTG
CTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTC
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTC
TGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACG
GAATAAATGTTTTCTCATTCAAAG

FIGURE 61

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24810, pI: 4.75, NX(S/T): 1
MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCVFN
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWFVGFC
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

Important features:
Type II Transmembrane domain:
amino acids 24-43

Other transmembrane domains:
amino acids 74-90, 108-126 and 145-161

N-glycosylation site.
amino acids 97-100

FIGURE 62

GAGCCACCTACCCTGCTCCGAGGCCAGGCCTGCAGGGCCTCATCGGCCAGAGGGTGATCAGT
GAGCAGAAGGATGCCCGTGGCCGAGGCCCCCCAGGTGGCTGGCGGGCAGGGGGACGGAGGTG
ATGGCGAGGAAGCGGAGCCAGAGGGGATGTTCAAGGCCTGTGAGGACTCCAAGAGAAAAGCC
CGGGGCTACCTCCGCCTGGTGCCCCTGTTTGTGCTGCTGGCCCTGCTCGTGCTGGCTTCGGC
GGGGGTGCTACTCTGGTATTTCCTAGGGTACAAGGCGGAGGTGATGGTCAGCCAGGTGTACT
CAGGCAGTCTGCGTGTACTCAATCGCCACTTCTCCCAGGATCTTACCCGCCGGGAATCTAGT
GCCTTCCGCAGTGAAACCGCCAAAGCCCAGAAGATGCTCAAGGAGCTCATCACCAGCACCCG
CCTGGGAACTTACTACAACTCCAGCTCCGTCTATTCCTTTGGGGAGGGACCCCTCACCTGCT
TCTTCTGGTTCATTCTCCAAATCCCCGAGCACCGCCGGCTGATGCTGAGCCCCGAGGTGGTG
CAGGCACTGCTGGTGGAGGAGCTGCTGTCCACAGTCAACAGCTCGGCTGCCGTCCCCTACAG
GGCCGAGTACGAAGTGGACCCCGAGGGCCTAGTGATCCTGGAAGCCAGTGTGAAAGACATAG
CTGCATTGAATTCCACGCTGGGTTGTTACCGCTACAGCTACGTGGGCCAGGGCCAGGTCCTC
CGGCTGAAGGGGCCTGACCACCTGGCCTCCAGCTGCCTGTGGCACCTGCAGGGCCCCAAGGA
CCTCATGCTCAAACTCCGGCTGGAGTGGACGCTGGCAGAGTGCCGGGACCGACTGGCCATGT
ATGACGTGGCCGGGCCCCTGGAGAAGAGGCTCATCACCTCGGTGTACGGCTGCAGCCGCCAG
GAGCCCGTGGTGGAGGTTCTGGCGTCGGGGGCCATCATGGCGGTCGTCTGGAAGAAGGGCCT
GCACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTTCCAGGCCTGTGAAG
TGAACCTGACGCTGGACAACAGGCTCGACTCCCAGGGCGTCCTCAGCACCCCGTACTTCCCC
AGCTACTACTCGCCCCAAACCCACTGCTCCTGGCACCTCACGGTGCCCTCTCTGGACTACGG
CTTGGCCCTCTGGTTTGATGCCTATGCACTGAGGAGGCAGAAGTATGATTTGCCGTGCACCC
AGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCCTACGCC
GAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGATCTCCCT
CACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTACAACCAGTCGGACCCCTGCCCTGGAG
AGTTCCTCTGTTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGACTGCCCC
AACGGCCTGGATGAGAGAAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGACAGCAC
ATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCGATGAAG
AGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTCACCTTCCAGTGTGAGGACCGGAGCTGC
GTGAAGAAGCCCAACCCGCAGTGTGATGGGCGGCCCGACTGCAGGGACGGCTCGGATGAGGA
GCACTGTGACTGTGGCCTCCAGGGCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGTCCTCCG
AGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCGGGGTCGACACATCTGTGGGGGGGCC
CTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCATGGCCTC
CACGGTGCTGTGGACCGTGTTCCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTGGAGAGG
TGTCCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCATGACTAC
GACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCGCTCGGCCGCCGTGCGCCCCGTCTG
CCTGCCCGCGCGCTCCCACTTCTTCGAGCCCGGCCTGCACTGCTGGATTACGGGCTGGGGCG
CCTTGCGCGAGGGCGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTGATCCCA
CAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGCCGGCTA
CCGCAAGGGCAAGAAGGATGCCTGTCAGGGTGACTCAGGTGGTCCGCTGGTGTGCAAGGCAC
TCAGTGGCCGCTGGTTCCTGGCGGGGCTGGTCAGCTGGGGCCTGGGCTGTGGCCGGCCTAAC
TACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGTGACCTG
AGGAACTGCCCCCCTGCAAAGCAGGGCCCACCTCCTGGACTCAGAGAGCCCAGGGCAACTGC
CAAGCAGGGGGACAAGTATTCTGGCGGGGGGTGGGGGAGAGAGCAGGCCCTGTGGTGGCAGG
AGGTGGCATCTTGTCTCGTCCCTGATGTCTGCTCCAGTGATGGCAGGAGGATGGAGAAGTGC
CAGCAGCTGGGGGTCAAGACGTCCCCTGAGGACCCAGGCCCACACCCAGCCCTTCTGCCTCC
CAATTCTCTCTCCTCCGTCCCCTTCCTCCACTGCTGCCTAATGCAAGGCAGTGGCTCAGCAG
CAAGAATGCTGGTTCTACATCCCGAGGAGTGTCTGAGGTGCGCCCCACTCTGTACAGAGGCT
GTTTGGGCAGCCTTGCCTCCAGAGAGCAGATTCCAGCTTCGGAAGCCCCTGGTCTAACTTGG
GATCTGGGAATGGAAGGTGCTCCCATCGGAGGGGACCCTCAGAGCCCTGGAGACTGCCAGGT
GGGCCTGCTGCCACTGTAAGCCAAAAGGTGGGGAAGTCCTGACTCCAGGGTCCTTGCCCCAC
CCCTGCCTGCCACCTGGGCCCTCACAGCCCAGACCCTCACTGGGAGGTGAGCTCAGCTGCCC
TTTGGAATAAAGCTGCCTGATCAAAAAAAAAAAAAAAAAAAAA

FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152
><subunit 1 of 1, 802 aa, 1 stop
><MW: 88846, pI: 6.41, NX(S/T): 7
MPVAEAPQVAGGQGDGGDGEEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT
YYNSSSVYSFGEGPLTCFFWFILQIPEHRRLMLSPEVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGQVLRLKGPDHLASSCLWHLQGPKDLML
KLRLEWTLAECRDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY
YDPFVLSVQPVVFQACEVNLTLDNRLDSQGVLSTPYFPSYYSPQTHCSWHLTVPSLDYGLAL
WFDAYALRRQKYDLPCTQGQWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS
LPKVCDGQPDCLNGSDEEQCQEGVPCGTFTFQCEDRSCVKKPNPQCDGRPDCRDGSDEEHCD
CGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIADRWVITAAHCFQEDSMASTVL
WTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPA
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG
KKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIQQVVT

Important features:
Type II transmembrane domain:
amino acids 46-67

Serine proteases, trypsin family, histidine active site.
amino acids 604-609

N-glycosylation sites.
amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447 and 509-512

Kringle domains.
amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:
amino acids 568-779

Homologous region to Low-density lipoprotein receptor:
amino acids 451-567

FIGURE 64

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT
CTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTACAACCAGTCGGACCCCTGCC
CTGGAGAGTTCCTCTGTTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC
TGCCCCAACGGCCTGGATGAGAGAAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGA
CAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTCACCTTCCAGTGTGAGGACCGG
AGCTGCGTGAAGAAGCCCAACCCGCAGTGTGATGGGCGGCCCGACTGCAGGGACGGCTCGGA
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCGGGGTCGACACATCTGTGGG
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT
GGCCTCCACGGTGCTGTGGACCGTGTTCCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG
GAGAGGTGTCCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT
GACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCGCTCGGCCGCCGTGCGCCC
CGTCTGCCTGCCCGCGCGCTCCCACTTCTTCGAGCCCGGCCTGCACTGCTGGATTACGGGCT
GGGGCGCCTTGCGCGAGGGCGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG
ATCCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC
CGGCTACCGCAAGGGCAAGAAGGATGCCTGTCAGGGTGACTCAGGTGGTCCGCTGGTGTGCA
AGGCACTCAGTGGCCGCTGGTTCCTGGCGGGGCTGGTCAGCTGGGGCCTGGGCTGTGGCCGG
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT
GACCTGAGGAACTGCCCCCCTGCAAAGCAGGGCCCACCTCCTGGACTCAGAGAGCCCAGGGC
AACTGCCAAGCAGGGGGACAAGTAT

FIGURE 65

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG
CTCCGTGCCGCCAAGTTTTCATTTTCCACCTTCTCTGCCTCCAGTCCCCCAGCCCCTGGCCG
AGAGAAGGGTCTTACCGGCCGGGATTGCTGGAAACACCAAGAGGTGGTTTTTGTTTTTTAAA
ACTTCTGTTTCTTGGGAGGGGGTGTGGCGGGGCAGGATGAGCAACTCCGTTCCTCTGCTCTG
TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC
GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG
TTTAACCTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTCGGCCACAG
CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAACCTTTTTCATCATTCACGGAT
GGACGATGAGCGGTATCTTTGAAAACTGGCTGCACAAACTCGTGTCAGCCCTGCACACAAGA
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCACCAGCTTTACACGGA
TGCGGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG
AGAAGGACGATTTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG
GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGGATCCTGC
CGGGCCCATGTTTGAAGGGGCCGACATCCACAAGAGGCTCTCTCCGGACGATGCAGATTTTG
TGGATGTCCTCCACACCTACACGCGTTCCTTCGGCTTGAGCATTGGTATTCAGATGCCTGTG
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGT
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAAATGTGAGCATGAGCGAGCCG
TCCACCTCTTTGTTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTGCCTTCCAGTGCACT
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCAT
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGG
CAGGCATGCCTTTCAGAGGTAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA
CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCACATCCTAGCCCAGGAGAAGTGGCCAGCA
CAATCCAATCAAATCGTTGCAAATCAGATTACACTGTGCATGTCCTAGGAAAGGAATCTTT
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646
><subunit 1 of 1, 354 aa, 1 stop
><MW: 39362, pI: 8.35, NX(S/T): 2
MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRTSKDPEHE
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVVDWL
PLAHQLYTDAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV
GRITGLDPAGPMFEGADIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLVNQDKPSFAFQCTDSNRFKKGICLS
CRKNRCNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

Important features:
Signal peptide:
amino acids 1-16

Lipases, serine active site.
amino acids 163-172

N-glycosylation sites.
amino acids 80-83 and 136-139

FIGURE 67

CGGACGCGTGGGCGGACGCGTGGGCCTGGGCAAGGGCCGGGGCGCCGGGCCGAGCCACCTCT
TCCCCTCCCCCGCTTCCCTGTCGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCA
CCCGGCCGGCCCTGGGGGCTGACAGTCGGCAAAGTTTGGCCCGAAGAGGAAGTGGTCTCAAA
CCCCGGCAGGTGGCGACCAGGCCAGACCAGGGGCGCTCGCTGCCTGCGGGCGGGCTGTAGGC
GAGGGCGCGCCCCAGTGCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAGAGAAGAGTGC
GGCGGCGGACGGAGAAAACAACTCCAAAGTTGGCGAAAGGCACCGCCCCTACTCCCGGGCTG
CCGCCGCCTCCCCGCCCCCAGCCCTGGCATCCAGAGTACGGGTCGAGCCCGGGCCATGGAGC
CCCCCTGGGGAGGCGGCACCAGGGAGCCTGGGCGCCCGGGGCTCCGCCGCGACCCCATCGGG
TAGACCACAGAAGCTCCGGGACCCTTCCGGCACCTCTGGACAGCCCAGGATGCTGTTGGCCA
CCCTCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAGACCGGATTATTTTTCCAAAT
CATGCTTGTGAGGACCCCCCAGCAGTGCTCTTAGAAGTGCAGGGCACCTTACAGAGGCCCCT
GGTCCGGGACAGCCGCACCTCCCCTGCCAACTGCACCTGGCTCATCCTGGGCAGCAAGGAAC
AGACTGTCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCCTA
CGCTCCCCTCTCCAGCCACTGATCTCCCTGTGTGAGGCACCTCCCAGCCCTCTGCAGCTGCC
CGGGGGCAACGTCACCATCACTTACAGCTATGCTGGGGCCAGAGCACCCATGGGCCAGGGCT
TCCTGCTCTCCTACAGCCAAGATTGGCTGATGTGCCTGCAGGAAGAGTTTCAGTGCCTGAAC
CACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCTGTGGCGATGGCTCTGA
TGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCCCTCCCTGC
CTTGCAATGTCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTA
GCCTCAGTCTCCCACCCCCAGTCCTGCCATTGGCTGCTGGACCCCCATGATGGCCGGCGGCT
GGCCGTGCGCTTCACAGCCCTGGACTTGGGCTTTGGAGATGCAGTGCATGTGTATGACGGCC
CTGGGCCCCCTGAGAGCTCCCGACTACTGCGTAGTCTCACCCACTTCAGCAATGGCAAGGCT
GTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGTCCTACCACACAGTTGCTTGGAGCAA
TGGTCGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCCTTGGGACAGACCCT
GTGGCTTAGGCTCTGGCCTGGGAGCTGGCGAAGGCCTAGGTGAGCGCTGCTACAGTGAGGCA
CAGCGCTGTGACGGCTCATGGGACTGTGCTGACGGCACAGATGAGGAGGACTGCCCAGGCTG
CCCACCTGGACACTTCCCCTGTGGGGCTGCTGGCACCTCTGGTGCCACAGCCTGCTACCTGC
CTGCTGACCGCTGCAACTACCAGACTTTCTGTGCTGATGGAGCAGATGAGAGACGCTGTCGG
CATTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCGTGTATGAGACGTGGGTGTG
CGATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCC
GCAAGGTCATTACAGCTGCAGTCATTGGCAGCCTAGTGTGCGGCCTGCTCCTGGTCATCGCC
CTGGGCTGCACCTGCAAGCTCTATGCCATTCGCACCCAGGAGTACAGCATCTTTGCCCCCCT
CTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCCCCTTCCTACGGGCAGCTCATTG
CCCAGGGTGCCATCCCACCTGTAGAAGACTTTCCTACAGAGAATCCTAATGATAACTCAGTG
CTGGGCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCC
AGGTGCCCGCCGTCGTCAGCGGGGCCGCTTGATGCGACGCCTGGTACGCCGTCTCCGCCGCT
GGGGCTTGCTCCCTCGAACCAACACCCCGGCTCGGGCCTCTGAGGCCAGATCCCAGGTCACA
CCTTCTGCTGCTCCCCTTGAGGCCCTAGATGGTGGCACAGGTCCAGCCCGTGAGGGCGGGGC
AGTGGGTGGGCAAGATGGGGAGCAGGCACCCCCACTGCCCATCAAGGCTCCCCTCCCATCTG
CTAGCACGTCTCCAGCCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCACTGCCC
CTAGAGCCATCACTATTGTCTGGAGTGGTGCAGGCCCTGCGAGGCCGCCTGTTGCCCAGCCT
GGGGCCCCCAGGACCAACCCGGAGCCCCCCTGGACCCCACACAGCAGTCCTGGCCCTGGAAG
ATGAGGACGATGTGCTACTGGTGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAG
GATGAGCCACTGCTTACCTGAGGGGACCTGGGGGCTCTACTGAGGCCTCTCCCCTGGGGGCT
CTACTCATAGTGGCACAACCTTTTAGAGGTGGGTCAGCCTCCCCTCCACCACTTCCTTCCCT
GTCCCTGGATTTCAGGGACTTGGTGGGCCTCCCGTTGACCCTATGTAGCTGCTATAAAGTTA
AGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACA
CCCCAGTCCCTTCACCACCACCTGCTCCCCACGCCACCACCATTTGGGTGGCTGTTTTTAAA
AAGTAAAGTTCTTAGAGGATCATAGGTCTGGACACTCCATCCTTGCCAAACCTCTACCCAAA
AGTGGCCTTAAGCACCGGAATGCCAATTAACTAGAGACCCTCCAGCCCCCAAGGGGAGGATT
TGGGCAGAACCTGAGGTTTTGCCATCCACAATCCCTCCTACAGGGCCTGGCTCACAAAAAGA
GTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAA
AGGAATCATACATCTC

FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631
<subunit 1 of 1, 713 aa, 1 stop
<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHPDRIIFPNHACEDPPAVLLEVQGTLQRPLVRDSRTSPANCTWLIL
GSKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAP
MGQGFLLSYSQDWLMCLQEEFQCLNHRCVSAVQRCDGVDACGDGSDEAGCSSDPFPGLTPRP
VPSLPCNVTLEDFYGVFSSPGYTHLASVSHPQSCHWLLDPHDGRRLAVRFTALDLGFGDAVH
VYDGPGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLP
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGAT
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRCRDEKCVYETWVCDGQPDCADGSDEWDCS
YVLPRKVITAAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY
GQLIAQGAIPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQRGRLMRRLVR
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKA
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLLPSLGPPGPTRSPPGPHTAV
LALEDEDDVLLVPLAEPGVWVAEAEDEPLLT

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA
GACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTGTGAAAGG
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC
AAGCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATA
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATAT
TATCAACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAA
GCCTGTGCATGAAAAAAAAGAAGTTTTGTAATTTTATATTACTTTTTAGTTTGATACTAAGT
ATTAAACATATTTCTGTATTCTTCCAAAAAAAAAAAAAAAAA

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645
><subunit 1 of 1, 152 aa, 1 stop
><MW: 17170, pI: 9.62, NX(S/T): 1
MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTFFIIAQAPEPYIVITGFEVTVILFFILL
YVLRLDRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTLTVGGGVFALVTAVCCLAD
GALIYRKLLFNPSGPYQKKPVHEKKEVL

Important features:

Potential type II transmembrane domain:
amino acids 26-42

Other potential transmembrane domain:
amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern
amino acids 78-99 and 85-106

N-myristoylation site.
amino acids 110-115

Ribonucleotide reductase large subunit protein
amino acids 116-127

FIGURE 71

GGGCGAGAAGTAGGGGAGGGCGTGTTCCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAGCCCC
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATACTTTTAT
ATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATATTATCAAC
TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTNTTGCCGAC

FIGURE 72

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG
CTGGGCGCGCCCCCCGGGCCCCGCCGTGGGCATGGGCGCACTGGCCCGGGCGCTGCTGCTGC
CTCTGCTGGCCCAGTGGCTCCTGCGCGCCGCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTG
CCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCC
TGCCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG
GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC
CTGGAGATGCTGATCGGGACCCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG
TAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT
CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAA
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATAC
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC
CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTG
AAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC
CATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGG
AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG
CTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCT
GAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTCAGC
CCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCATCCACAAAT
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAA
GAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT
CCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG
CCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT
AATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCA
ATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA
CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG
CTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATTCAC
TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA
AAAAAAAACTTCATTCTAA

FIGURE 73

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493
><subunit 1 of 1, 518 aa, 1 stop
><MW: 56180, pI: 5.08, NX(S/T): 2

MGALARALLLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGLAL
ALEPALASPAGAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS
YIDTYFDTERSSTYRSKGFDVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENF
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS
LVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLR
LPQKVFDAVVEAVARASLIPEFSDGFWTGSQLACWTNSETPWSYFPKISIYLRDENSSRSFR
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLIVLLLLPFRC
QRRPRDPEVVNDESSLVRHRWK

Important features:

Signal peptide:
amino acids 1-20

Transmembrane domain:
amino acids 466-494

N-glycosylation sites.
amino acids 170-173 and 366-369

Leucine zipper pattern.
amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases
amino acids 109-118, 252-261 and 298-310

FIGURE 74

CGCCTCCGCCTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG
GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGGCCTGGGCGGAGCCGGGAGGCGCGGCC
GGC<u>ATG</u>GAGGCGCTGCTGCTGGGCGCGGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA
CAACCTGGTGAAGGCCCCGCCGTGCGGCGGCATGGGCAACCTGCGGGGCCGCACGGCCGTGG
TCACGGGCGCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG
CGCGTGGTGCTGGCCTGCCGCAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA
GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC
GGTATCAGTTCCTGTGGCCGGACCCGTGAGGCGTTTAACCTGCTGCTTCGGGTGAACCATAT
CGGTCCCTTTCTGCTGACACATCTGCTGCTGCCTTGCCTGAAGGCATGTGCCCCTAGCCGCG
TGGTGGTGGTAGCCTCAGCTGCCCACTGTCGGGGACGTCTTGACTTCAAACGCCTGGACCGC
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT
GTTTGCCCGGGAGCTCGCCAACCAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCCACC
CAGGGCCTGTGAACTCGGAGCTGTTCCTGCGCCATGTTCCTGGATGGCTGCGCCCACTTTTG
CGCCCATTGGCTTGGCTGGTGCTCCGGGCACCAAGAGGGGGTGCCCAGACACCCCTGTATTG
TGCTCTACAAGAGGGCATCGAGCCCCTCAGTGGGAGATATTTTGCCAACTGCCATGTGGAAG
AGGTGCCTCCAGCTGCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG
CTGGCAGGGCTTGGGCCTGGGGAGGATGCTGAACCCGATGAAGACCCCCAGTCTGAGGACTC
AGAGGCCCCATCTTCTCTAAGCACCCCCCACCCTGAGGAGCCCACAGTTTCTCAACCTTACC
CCAGCCCTCAGAGCTCACCAGATTTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG
CCTGAGATCCAGCTCTCC<u>TAA</u>CCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCTT
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCCTGGTTGAAGGAAT
AATGGGTGATTATTTCTTCCTGAGAGTGACAGTAACCCCAGATGGAGAGATAGGGGTATGCT
AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCCTTATTGATTCTG
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG
TGAACTGATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCCATGTTAATGAAGCG
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG
GGATCTGAACCCAAGGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG
ATGCAGGGCTGGGGTCATCTGTATCTGAAGCCCCTCGGAATAAAGCGCGTTGACCGCCAAAA
AAAAAAAAAAAAAAAA

FIGURE 75

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227
<subunit 1 of 1, 377 aa, 1 stop
<MW: 40849, pI: 7.98, NX(S/T): 0
MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSGIGKMTALELARRGAR
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG
ISSCGRTREAFNLLLRVNHIGPFLLTHLLLPCLKACAPSRVVVVASAAHCRGRLDFKRLDRP
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPVNSELFLRHVPGWLRPLLR
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDDRAAHRLWEASKRL
AGLGPGEDAEPDEDPQSEDSEAPSSLSTPHPEEPTVSQPYPSPQSSPDLSKMTHRIQAKVEP
EIQLS

Important features:
Signal peptide:
amino acids 1-16

Glycosaminoglycan attachment site.
amino acids 46-49

Short-chain alcohol dehydrogenase family
amino acids 37-49 and 114-124

FIGURE 76A

GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATGGG
AGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTCCAGG
GCCCTGGCCCTGCCAGGATGAGCTGCCAAGCCTCAGGCCAGCCACCTCCCACCATCCGCTGG
TTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCTGCCTGATGG
GACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCAGGCCCTGTCCA
CAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGC
GCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTGGC
TGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGGCCACCCAGAGCCCACAG
TCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGGAAGGCACACAGTGTCCGGG
GGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGGGACCTACATGTGTGTGGCCAC
CAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGGTTTCCATCCAGGAGCCCCAGGACT
ACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAAAATGTGACACTGCTGAAC
CCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGGCGGTGTGGCTCAGCTGGAAGGTCAGTGG
CCCTGCTGCGCCTGCCCAATCTTACACGGCCTTGTTCAGGACCCAGACTGCCCCGGGAGGCC
AGGGAGCTCCGTGGGCAGAGGAGCTGCTGGCCGGCTGGCAGAGCGCAGAGCTTGGAGGCCTC
CACTGGGGCCAAGACTACGAGTTCAAAGTGAGACCATCCTCTGGCCGGGCTCGAGGCCCTGA
CAGCAACGTGCTGCTCCTGAGGCTGCCGGAAAAAGTGCCCAGTGCCCCACCTCAGGAAGTGA
CTCTAAAGCCTGGCAATGGCACTGTCTTTGTGAGCTGGGTCCCACCACCTGCTGAAAACCAC
AATGGCATCATCCGTGGCTACCAGGTCTGGAGCCTGGGCAACACATCACTGCCACCAGCCAA
CTGGACTGTAGTTGGTGAGCAGACCCAGCTGGAAATCGCCACCCATATGCCAGGCTCCTACT
GCGTGCAAGTGGCTGCAGTCACTGGTGCTGGAGCTGGGGAGCCCAGTAGACCTGTCTGCCTC
CTTTTAGAGCAGGCCATGGAGCGAGCCACCCAAGAACCCAGTGAGCATGGTCCCTGGACCCT
GGAGCAGCTGAGGGCTACCTTGAAGCGGCCTGAGGTCATTGCCACCTGCGGTGTTGCACTCT
GGCTGCTGCTTCTGGGCACCGCCGTGTGTATCCACCGCCGGCGCCGAGCTAGGGTGCACCTG
GGCCCAGGTCTGTACAGATATACCAGTGAGGATGCCATCCTAAAACACAGGATGGATCACAG
TGACTCCCAGTGGTTGGCAGACACTTGGCGTTCCACCTCTGGCTCTCGGGACCTGAGCAGCA
GCAGCAGCCTCAGCAGTCGGCTGGGGGCGGATGCCCGGGACCCACTAGACTGTCGTCGCTCC
TTGCTCTCCTGGGACTCCCGAAGCCCCGGCGTGCCCCTGCTTCCAGACACCAGCACTTTTTA
TGGCTCCCTCATCGCTGAGCTGCCCTCCAGTACCCCAGCCAGGCCAAGTCCCCAGGTCCCAG
CTGTCAGGCGCCTCCCACCCCAGCTGGCCCAGCTCTCCAGCCCCTGTTCCAGCTCAGACAGC
CTCTGCAGCCGCAGGGGACTCTCTTCTCCCCGCTTGTCTCTGGCCCCTGCAGAGGCTTGGAA
GGCCAAAAAGAAGCAGGAGCTGCAGCATGCCAACAGTTCCCCACTGCTCCGGGGCAGCCACT
CCTTGGAGCTCCGGGCCTGTGAGTTAGGAAATAGAGGTTCCAAGAACCTTTCCCAAAGCCCA
GGAGCTGTGCCCCAAGCTCTGGTTGCCTGGCGGGCCCTGGGACCGAAACTCCTCAGCTCCTC
AAATGAGCTGGTTACTCGTCATCTCCCTCCAGCACCCCTCTTTCCTCATGAAACTCCCCCAA
CTCAGAGTCAACAGACCCAGCCTCCGGTGGCACCACAGGCTCCCTCCTCCATCCTGCTGCCA
GCAGCCCCCATCCCCATCCTTAGCCCCTGCAGTCCCCCTAGCCCCCAGGCCTCTTCCCTCTC
TGGCCCCAGCCCAGCTTCCAGTCGCCTGTCCAGCTCCTCACTGTCATCCCTGGGGGAGGATC
AAGACAGCGTGCTGACCCCTGAGGAGGTAGCCCTGTGCTTGGAACTCAGTGAGGGTGAGGAG
ACTCCCAGGAACAGCGTCTCTCCCATGCCAAGGGCTCCTTCACCCCCCACCACCTATGGGTA
CATCAGCGTCCCAACAGCCTCAGAGTTCACGGACATGGGCAGGACTGGAGGAGGGGTGGGGC
CCAAGGGGGGAGTCTTGCTGTGCCCACCTCGGCCCTGCCTCACCCCCACCCCCAGCGAGGGC
TCCTTAGCCAATGGTTGGGGCTCAGCCTCTGAGGACAATGCCGCCAGCGCCAGAGCCAGCCT
TGTCAGCTCCTCCGATGGCTCCTTCCTCGCTGATGCTCACTTTGCCCGGGCCCTGGCAGTGG
CTGTGGATAGCTTTGGTTTCGGTCTAGAGCCCAGGGAGGCAGACTGCGTCTTCATAGATGCC
TCATCACCTCCCTCCCCACGGGATGAGATCTTCCTGACCCCCAACCTCTCCCTGCCCCTGTG
GGAGTGGAGGCCAGACTGGTTGGAAGACATGGAGGTCAGCCACACCCAGCGGCTGGGAAGGG
GGATGCCTCCCTGGCCCCCTGACTCTCAGATCTCTTCCCAGAGAAGTCAGCTCCACTGTCGT
ATGCCCAAGGCTGGTGCTTCTCCTGTAGATTACTCCTGAACCGTGTCCCTGAGACTTCCCAG
ACGGGAATCAGAACCACTTCTCCTGTCCACCCACAAGACCTGGGCTGTGGTGTGTGGGTCTT
GGCCTGTGTTTCTCTGCAGCTGGGGTCCACCTTCCCAAGCCTCCAGAGAGTTCTCCCTCCAC
GATTGTGAAAACAAATGAAAACAAAATTAGAGCAAAGCTGACCTGGAGCCCTCAGGGAGCAA
AACATCATCTCCACCTGACTCCTAGCCACTGCTTTCTCCTCTGTGCCATCCACTCCCACCAC
CAGGTTGTTTTGGCCTGAGGAGCAGCCCTGCCTGCTGCTCTTCCCCCACCATTTGGATCACA

FIGURE 76B

GGAAGTGGAGGAGCCAGAGGTGCCTTTGTGGAGGACAGCAGTGGCTGCTGGGAGAGGGCTGT
GGAGGAAGGAGCTTCTCGGAGCCCCCTCTCAGCCTTACCTGGGCCCCTCCTCTAGAGAAGAG
CTCAACTCTCTCCCAACCTCACCATGGAAAGAAAATAATTATGAATGCCACTGAGGCACTGA
GGCCCTACCTCATGCCAAACAAAGGGTTCAAGGCTGGGTCTAGCGAGGATGCTGAAGGAAGG
GAGGTATGAGACCGTAGGTCAAAAGCACCATCCTCGTACTGTTGTCACTATGAGCTTAAGAA
ATTTGATACCATAAAATGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 77

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404
<subunit 1 of 1, 985 aa, 1 stop
<MW: 105336, pI: 6.55, NX(S/T): 7
MGGMAQDSPPQILVHPQDQLFQGPGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHHLLP
DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEGTYMCV
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLSWKV
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG
PDSNVLLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGPW
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST
FYGSLIAELPSSTPARPSPQVPAVRRLPPQLAQLSSPCSSSDSLCSRRGLSSPRLSLAPAEA
WKAKKKQELQHANSSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS
SSNELVTRHLPPAPLFPHETPPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPPSPQASS
LSGPSPASSRLSSSSLSSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPPRPCLTPTPSEGSLANGWGSASEDNAASARA
SLVSSSDGSFLADAHFARALAVAVDSFGFGLEPREADCVFIDASSPPSPRDEIFLTPNLSLP
LWEWRPDWLEDMEVSHTQRLGRGMPPWPPDSQISSQRSQLHCRMPKAGASPVDYS

Important features:

Transmembrane domain:

amino acids 448-467

N-glycosylation sites:

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

N-myristoylation sites.

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

Phosphotyrosine interaction domain proteins

amino acids 740-753

FIGURE 78

CTCCCACGGTGTCCAGCGCCCAGAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCT
CCCAGGTTATGAAGCCCTGGAGGGCCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT
GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGA
ACCTCACCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
TCTTTACTGATCTCTCTGTTCGTCTTTCCAGGACCCTGCTGTCCTCCCTCCCCTTCTCCCAC
CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCC
CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
GCTGAGGCCCCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCCATGCAGC
TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCCTGGTGCTGCTGAGCCTTCTGTCAGC
CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA
CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCC
CCTTCCCAGGCCCCTGAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA
GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT
GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAG
TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGCATGTTCCA
GCCTGACCTAGAAGCGTTTGTCAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG
GAGACTGGGACATCCCTGATAGGTTCACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA
GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACTCCTGGGC
CTCATGCCCAGTGTCGGACCCTGCCTTCCTCCCACTCCAGACCCCACCTTGTCTTCCCTCCC
TGGCGTCCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT
GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT
GTGAAAAACGTGATTCCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
GACTCTGAATTCTAACAATGCCCAGTGACTGTCGCACTTGAGTTTGAGGGCCAGTGGGCCTG
ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCC
CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCCTGCTAAG
TCCAGGCCTTGGTCAGGTCAGGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG
TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCCTTTGGAAAAAATGATGAAGA
AAACCTTGGCTCCTTCCTTGTCTGGAAAGGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA
GAAAAGTAGAAAACCAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTCGGGGGTGGTGGTAAAGTA
GCACAACTACTATTTTTTTTCTTTTTCCATTATTATTGTTTTTTAAGACAGAATCTCGTGCT
GCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACTCCGCCTCCTGGGTTCAAGTGATT
CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT
TTTGTACTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAACTCCTGAC
CTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG
TCTGGCCCTATTTCCTTTAAAAGTGAAATTAAGAGTTGTTCAGTATGCAAAACTTGGAAAG
ATGGAGGAGAAAAAGAAAAGGAAGAAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT
TATTTCGTTTTGTTGTACTTCCTTCCACTCTTTTCTTCTTCACATAATTTGCCGGTGTTCTT
TTTACAGAGCAATTATCTTGTATATACAACTTTGTATCCTGCCTTTTCCACCTTATCGTTCC
ATCACTTTATTCCAGCACTTCTCTGTGTTTTACAGACCTTTTTATAAATAAAATGTTCATCA
GCTGCATAAAAAAAAAAAAAA

FIGURE 79

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196
<subunit 1 of 1, 332 aa, 1 stop
<MW: 36143, pI: 5.89, NX(S/T): 1
MRLLVLLWGCLLLPGYEALEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSIRDSRQELSLIVTLWNLTLQDAGEYWCGVEKRGPDESLLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAEEKEAPSQAPEGD
VISMPPLHTSEEELGFSKFVSA

Important features:

Signal peptide:
amino acids 1-17

Transmembrane domain:
amino acids 248-269

N-glycosylation site.
amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.
amino acids 104-113

Ig like V-type domain:
amino acids 13-128

FIGURE 80

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGTGGCAGGA
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC
GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCATCCCAA
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG
CAGGGCTCTCAGAAGGCGGTGGTGCCCAGCTGGGATC<u>ATG</u>TTGTTGGCCCTGGTCTGTCTGC
TCAGCTGCCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC
TTATTTCACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCGAACGTCCCCAAC
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCC
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTC<u>TAG</u>GATGGACGGAACCATGCA
CAGCAGGCTGGGAAATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA
AAGGATGGTTGAACGTGAAA

FIGURE 81

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187
<subunit 1 of 1, 146 aa, 1 stop
<MW: 16430, pI: 5.05, NX(S/T): 1
MLLALVCLLSCLLPSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD
YEADGSTNNGIFQINSRRWCSNLTPNVPNVCRMYCSDLLNPNLKDTVICAMKITQEPQGLGY
WEAWRHHCQGKDLTEWVDGCDF

Important features:
Signal peptide:
amino acids 1-18

N-myristoylation site.
amino acids 67-72

Homolgous region to Alpha-lactalbumin / lysozyme C proteins.
amino acids 34-58 (catalytic domain), 111-132 and 66-107

FIGURE 82

AGCCGCTGCCCCGGGCCGGGCGCCCGCGGCGGCACCATGAGTCCCCGCTCGTGCCTGCGTTC
GCTGCGCCTCCTCGTCTTCGCCGTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCA
AGCTGTCGTCGGTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAAACTCAAGGGCCTGATC
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAACCGGCGCTGGAACTGCTCCACAC
TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTG
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGCAGCAGTGGGGAGCT
GGAGAAGTGCGGCTGTGACAGGACAGTGCATGGGGTCAGCCCACAGGGCTTCCAGTGGTCAG
GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG
AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCCGGCAG
GAAGGCCATCCTGACACACATGCGGGTGGAATGCAAGTGCCACGGGGTGTCAGGCTCCTGTG
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTCACGCACTGAAGGAG
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACC
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG
ACTTCTGTGAGCAGGACATGCGCAGCGGCGTGCTGGGCACGAGGGGCCGCACATGCAACAAG
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGCGGCTTCCACACGGCGCA
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCCACTGGTGCTGCTTCGTCAAGTGCCGGC
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGACCGCCTGCCTAGCCCTGCGCCGGC
AACCACCTAGTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCCACCACCTACCCCAAGA
GATACTGGTTGTATTTTTTGTTCTGGTTTGGTTTTTGGGTCCTCATGTTATTTATTGCCGAA
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAAGCCTGGGCCTTTGTGGCT
GCCACTGACCAAAGGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTGGCTGCCACTGACCA
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTAT
TACCACCACATGGCTACTGACCGTGTCATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATA
GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAAGAACTCTTAACTCTCCAGCACACA
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG
GAACAAGCAGATACCAGGTCAAGGGCACCAGGTTCATTTCAGCCCTTACATGGACAGCTAGA
GGTTCGATATCTGTGGGTCCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA
GTCCCACCCTAGAACCCAGCCTGCCCCAGCCTGCCCCTGGGAAGAGGAAACTTAACCACTCC
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT
TGCAGTCATGCCCGAGTCACCTTTCACAGCGCTGTTCCTCCATGAAACTGAAAAACACACAC
ACACACACACACACACACACACACACACACACACACACGGACACACACACACACCTGCGAGA
GAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCCGAGTCACCTTTCACAGCACTGTTCCTC

FIGURE 83

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328
<subunit 1 of 1, 351 aa, 1 stop
<MW: 39052, pI: 8.97, NX(S/T): 2
MSPRSCLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVQMCKRNLE
VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSAGVAFAV
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKGASSSRALM
NLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC
CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

Important features:

Signal peptide:
amino acids 1-22

N-glycosylation sites.
amino acids 88-91 and 297-300

Wnt-1 family signature.
amino acids 206-215

Homologous region to Wnt-1 family proteins
amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT
CGCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTC
ACCACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGCGCTGG
GTGCCCTGAAGGAGGAGGTCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT
GCGGGAACTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACTCCTGCGAGCCG
TGCCCCACGTCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC
TGGATGAGCAGGGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGG
GCTGTGCGCCATCTGGGCAAGGTTCAGGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTT
CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTCATGATGC
TGCACACGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG
AAAAGGCACAACTGCTGACCCCGCCCAGTGCCCTGGAGCCGCGCCCATTGCAGCATGTCGTA
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTCTTCCT
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAACC
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACTGGA
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAAA

FIGURE 85

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352
<subunit 1 of 1, 293 aa, 1 stop
<MW: 32562, pI: 6.53, NX(S/T): 2
MDTTRYSKWGGSSEEVPGGPWGRWVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA
LLDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALR
ELRERVTQGLAEAGRGREDVRTELFRALEAVRLQNNSCEPCPTSWLSFEGSCYFFSVPKTTW
AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS
HWNQGEPNDAWGRENCVMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:

Type II transmembrane domain:
amino acids 31-54

N-glycosylation sites.
amino acids 73-76 and 159-162

Leucine zipper pattern.
amino acids 102-123

N-myristoylation sites.
amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.
amino acids 264-287

FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG
GCAGCCCCCGCCGCCCCCGCAGCCCCTTCTCCTCCTTTCTCCCACGTCCTATCTGCCTCTCG
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACTGGAGCCTCATTGGCCGGCCCGG
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC
CGCGCTCCCGCTGCTCCTGCCGGGTG<u>ATG</u>GAAAACCCCAGCCCGGCCGCCGCCCTGGGCAAG
GCCCTCTGCGCTCTCCTCCTGGCCACTCTCGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTC
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA
CGGCCTTCCCCAAGCAGTACCCCCTGTTCCGCCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTCAGTAACGGGCTGCG
CGACTTTGCGGAGCGCGGCGAGGCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGGAGG
CGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCGCCGTCCCCAGCGGCACCGGGCAGACG
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCC
CAGCCCCGACTGGTTCGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTCACCTTCTCC
TCCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCCTCTCCCAG
CCACCCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGA
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCCTGCCCAGC
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTC
CCTGTGGTCGTCCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA
CTCGCTACGTCCGGGTCCAGCCCGCCAACAACGGGAGCCCCTGCCCCGAGCTCGAAGAAGAG
GCTGAGTGCGTCCCTGATAACTGCGTC<u>TAA</u>GACCAGAGCCCCGCAGCCCCTGGGGCCCCCCG
GAGCCATGGGGTGTCGGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCACAGGG
GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT
CTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG
CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGTCCTTCATCG
TCCAGGGGCCTGGCTCCCACGTGGTTGCAGATACCTCAGACCTGGTGCTCTAGGCTGTGCTG
AGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAATAAATGGGGCGG
TTTCGGAAGCGTCAGTGTTTCCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT
GTTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 87

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35844, pI: 5.45, NX(S/T): 2
MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPL
FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALMKEIEAAGEALQSVHEVF
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYP
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP
RAFIPPAPVLPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTKSRTRYVRVQPA
NNGSPCPELEEEAECVPDNCV

Important features:
Signal peptide:
amino acids 1-26

FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGTCTTGCGTGA
TATTGACAAACTGAAGCTTTCCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGA
CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC
CAAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAATGGGAAGGTTTTATTGAAAACTA
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGCAGAAATTTT
ATCCAACTTTGTTTGGAAGCTTATTATGACAATACCATTTTTCATAGAGTTGTGCCTGGTTT
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC
CATTCAAAGATGAATTTCATTCACGGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCA
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACACTGGGTCGAGCAGATGAACT
TAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAAGCTGT
GAGGTTTTGTTTAATCCTTTTGATGACATCATTCCAAGGGAAATTAAAAGGCTGAAAAAAGA
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTTAGTTTACTTT
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT
TGTAGAAAGTGAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG
AGCATGATGAATATATTGATGGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAAA
TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC
AGTCAGCCGCAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAAAACGGGAACTCTTAGCAG
CAAAACAAAAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAAGAAGTGAAGAGGAAGAA
GCCCCTCCAGATGGTGCTGTTGCCGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAG
GAAGCAACAGTCAAAGAAGGGAACTTCCCGGGAAGATCAGACCCTTGCACTGCTGAACCAGT
TTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGAA
GTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGT
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA
ATAAAAGAAGGAGGGAAGAAAGCAAAAAGCTGATGAGAGAGAAAAAAGAAAGAAGATAAAAT
GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTTGTAACAGCCATTG
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTTGTCTGGTTTTG
AAAAACAATTATCTTGTTTTGCAAATTGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGG
TACATGTGTTTTTTCCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCCT
TCCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 89

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919
><subunit 1 of 1, 472 aa, 1 stop
><MW: 53847, pI: 5.75, NX(S/T): 2

MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYYDNTIFHRVVPGFI
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFNPFDDIIPREIKRLKKEK
PEEEVKKLKPKGTKNFSLLSFGEEAEEEEEEVNRVSQSMKGKSKSSHDLLKDDPHLSSVPVV
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKSV
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEEAPPDGAVAEYRREKQKYEALRK
QQSKKGTSREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMSHVLQFEDKSRKVK
DASMQDSDTFEIYDPRNPVNKRRREESKKLMREKKERR

Important features:

Signal peptide:
amino acids 1-21

N-glycosylation sites.
amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.
amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase
amino acids 96-140, 49-89 and 22-51

FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGG
CCCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCCAGACCCATTTCGCCTTGCTGACGGCGTCG
AGCCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC
GTGGCCGCCGGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAA
CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTG
CTCCTTCAAGTGGTTTTGGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA
GGAGGAACAAATACAGGTGCCTTGCACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAAC
CCTGCAAGGAAAACAGATGCATGTGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCT
TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAGCCCTGGAAA
GGAATCAGAGATGCTACCACCTACCCGCCTGGATGGAGTCTCGCTCTGTCGCCAGGCTGGAG
TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGAGTCTCCTGC
CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCCTGGGGCCAGCTGGCCTCG
ATGTACGTCAGCACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT
GAACGTGTACGCGCCGGCGCGCGCGCCCGGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCC
CGGGAGGCGCCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCCGC
GAGAAAGTGGTGCTGGTGTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGA
CGACAGCCACGCGCGCGGGAACTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGC
AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTCGGCCAGTCGGCG
GGGGCCATGAGCATCTCAGGACTGATGATGTCACCCCTAGCCTCGGGTCTCTTCCATCGGGC
CATTTCCCAGAGTGGCACCGCGTTATTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGG
CCAAGAAGGTTGCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC
CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCCTCCAACT
GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG
TGATCCCAGATGACCCTTTGGTGCTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT
CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCTTATAATATCACCAAGGAGCAGGT
ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA
ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGCTCAC
TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA
AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGC
TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC
TATGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGACTAGCCA
TGGACATACCTGGGGACAAGAGTTCTACCCACCCCAGTTTAGAACTGCAGGAGCTCCCTGCT
GCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGTTGTGTGGGACCTGCACTGCCCTTTCCAGCC
TGACATCCCATGATGCCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC
ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTTCCCTTCTTCAAATCCT
CCCACCCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGGTCGACCCAGACTGCCACTGC
CCCTGTCACTGCACCCAGCTTGGCATTTACCATCCATCCTGCTCAACCTTGTTCCTGTCTGT
TCACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACATGGAGCAAACTTTTGGTAGTTTGGGA
TCTTCTCTCCCACCCACACTTATCTCCCCCAGGGCCACTCCAAAGTCTATACACAGGGGTGG
TCTCTTCAATAAAGAAGTGTTGATTAGAAAAAAAAAAA

FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179
<subunit 1 of 1, 545 aa, 1 stop
<MW: 58934, pI: 9.45, NX(S/T): 4

MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTSAPSSG
FGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLQGKQMHVGKTPIQVFLGVPFSRPP
LGILRFAPPEPPEPWKGIRDATTYPPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVMVWFPGGAF
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA
AFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRFLQLNFQRDPEEIIWSMSPVVDGVVIPDD
PLVLLTQGKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMD
IVQDATFVYATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

FIGURE 92

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT
GCTGTCCTCGCTGCTGGGCGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG
AGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCCGA
CAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC
CAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCC
GATTCCAGCTCACTGGGGATCCCGCCAAGGGGAACTGCTCCTTGGTGATCAGAGACGCGCAG
ATGCAGGATGAGTCACAGTACTTCTTTCGGGTGGAGAGAGGAAGCTATGTGACATATAATTT
CATGAACGATGGGTTCTTTCTAAAAGTAACAGTGCTCAGCTTCACGCCCAGACCCCAGGACC
ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC
GTCCGACTCCGTGTGGCCTATGCCCCCAGAGACCTTGTTATCAGCATTTCACGTGACAACAC
GCCAGCCCTGGAGCCCCAGCCCCAGGGAAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGT
TCCTGCGGCTCCTCTGTGCTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCCTGCAG
AACAGAGTCCTCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGG
GGTGAAGGCTGGGGATTCAGGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGC
AGCGAGCCCTGGACCTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAA
GCAAACAGGACAGTCCTGGAAAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCA
AAGCCTGTGCCTGGTCTGTGTCACACACAGCAGCCCCCCAGCCAGGCTGAGCTGGACCCAGA
GGGGACAGGTTCTGAGCCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTT
CAAGTGGAGCACGAAGGAGAGTTCACCTGCCACGCTCGGCACCCACTGGGCTCCCAGCACGT
CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAG
CGTTTCTGGGAATCGGCATCACGGCTCTTCTTTTCCTCTGCCTGGCCCTGATCATCATGAAG
ATTCTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACAGCAC
GATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA
AAGCCACACCAAACAGTCCTCGGACCCCTCCTCCACCAGGTGCTCCCTCCCCAGAATCAAAG
AAGAACCAGAAAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACTCAAGC
CCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCA
GACCCAGGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTC
CAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGGTAGAGTAAGAG
GTTGAAGATAACAGAGTGCAAAGTTTCCTTCTCTCCCTCTCTCTCTCTCTTTCTCTCTCTCT
CTCTCTTTCTCTCTCTTTTAAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCTGTAATC
CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTCGGGAGTTCGAGACCAGCCTG
GCCAACTTGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCAGG
CGCCTGTAATCCTACCTACTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG
AGGTTGCAGTGAGCCAAGATCACACCATTGCACGCCAGCCTGGGCAACAAAGCGAGACTCCA
TCTCAAAAAAAAAATCCTCCAAATGGGTTGGGTGTCTGTAATCCCAGCACTTTGGGAGGCTA
AGGTGGGTGGATTGCTTGAGCCCAGGAGTTCGAGACCAGCCTGGGCAACATGGTGAAACCCC
ATCTCTACAAAAAATACAAAACATAGCTGGGCTTGGTGGTGTGTGCCTGTAGTCCCAGCTGT
CAGACATTTAAACCAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC
TACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGGTCCG
TACAAGATACAGGTCATAAAGACTTTGCTGATAAAACAGATTGCAGTAAAGAAGCCAACCAA
ATCCCACCAAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCGTCCTCACTGCTACACTCCT
GACAGCACCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA
AAAGGGGGAGGAATGAATAATCCACCCCTTGTTTAGCAAATAAGCAAGAAATAACCATAAAA
GTGGGCAACCAGCAGCTCTAGGCGCTGCTCTTGTCTATGGAGTAGCCATTCTTTTGTTCCTT
TACTTTCTTAATAAACTTGCTTTCACCTTAAAAAAA

FIGURE 93

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002
><subunit 1 of 1, 544 aa, 1 stop
><MW: 60268, pI: 9.53, NX(S/T): 3
MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFK
AVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGS
YVTYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPL
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSL
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHP
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPR
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

Important features:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

Immunoglobulins and major histocompatibility complex proteins signature.

amino acids 365-371

FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAACTGTTATTTACTGCTGCGTTT
TATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACTCTCAAACAAAGA
AAGTCAAGCAGCCAGTGCGATCTCATTTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT
TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA
CAATGGAAACAATTCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA
TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC
TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA
GTTTGTCATCAAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC
ATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC
TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
TCTGGAACAACAAGTGTATTAATTAAACTTTCAGATGTTAATGACAATAAGCCTATATTTAA
AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT
GATTCGCAAACATTTGACATTATTACTAATCATGAAACTCAAGAAGGAATAGTTATATTAAA
AAAGAAAGTGGATTTTGAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAACCATC
ATGTTCCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCACTTTCATTAAGATCCAG
GTGGAAGATGTTGATGAGCCTCCTCTTTTCCTCCTTCCATATTATGTATTTGAAGTTTTTGA
AGAAACCCCACAGGGATCATTTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT
CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCAATATCAATGATAATGGTACAATC
ACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAACATCA
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT
GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTT
TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAAGTTTTACAATCATAGATAATCAAG
ATAACACAGCTGTCATTTTGACTAATAGAACTGGTTTTAACCTTCAAGAAGAACCTGTCTTC
TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTTGCATTATGATCATA
TTTGGGTTTATTTTTTTGACTTTGGGTTTAAAACAACGGAGAAAACAGATTCTATTTCCTGA
GAAAAGTGAAGATTTCAGAGAGAATATATTCCAATATGATGATGAAGGGGGTGGAGAAGAAG
ATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT
CGGAAAACCACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA
CAGTGCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG
CCCCTCCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCC
CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT
GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAATTAGG
GCTTTTTACCATCAAAATTTTTAAAAGTGCTAATGTGTATTCGAACCCAATGGTAGTCTTAA
AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC
CTGGAGTAAATACTCCATGGTTATTTTAAGCTACCTACATGCTGTCATTGAACAGAGATGTG
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAAATAATG
TAGGAAGATATTAAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT
CATTATTTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAATTTAAAGGAGCAAAAATTTG
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCCATGAAGTATTGTTTCCTTTAT
TTAAA

FIGURE 95

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906

><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHH
IGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL
LYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSD
VNDNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
PYYVFEVFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
DESIEEHHFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP
SLTSTNTLTIHVCDCGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESAVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518, 516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

FIGURE 96

ATTTCAAGGCCAGCCATATTTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTTNTA
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAAACTTTCAGATGTTAATGACAA
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC
AGCATTGAAGAGGATGATTCGCAAACATTTGACATTATT

FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCCGGGCGCGGACCCCAACCCCGAC
CCAGAGCTTCTCCAGCGGCGGCGCAGCGAGCAGGGCTCCCCGCCTTAACTTCCTCCGCGGGG
CCCAGCCACCTTCGGGAGTCCGGGTTGCCCACCTGCAAACTCTCCGCCTTCTGCACCTGCCA
CCCCTGAGCCAGCGCGGGCCCCCGAGCGAGTCATGGCCAACGCGGGGCTGCAGCTGTTGGGC
TTCATTCTCGCCTTCCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCCAGTGGAG
GATTTACTCCTATGCCGGCGACAACATCGTGACCGCCCAGGCCATGTACGAGGGGCTGTGGA
TGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT
CTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGAT
AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGC
AGAAGATGAGGATGGCTGTCATTGGGGGTGCGATATTTCTTCTTGCAGGTCTGGCTATTTTA
GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCCCAGT
CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCC
TTCTGGGAGGTGCCCTACTTTGCTGTTCCTGTCCCCGAAAAACAACCTCTTACCCAACACCA
AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAAGACTACGTGTGACACAGAGGCAAAAG
GAGAAAATCATGTTGAAACAAACCGAAAATGGACATTGAGATACTATCATTAACATTAGGAC
CTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAACAAACAAACAAACAAAAA
ACCCATGTGTTAAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTTCCTCA
ATATAGGAGGGAAGATTTTTCCATTTGTATTACTGCTTCCCATTGAGTAATCATACTCAAAT
GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTTCTATTAAAA
ATAGACAGTAAAATACTATTCTCATTATGTTGATACTAGCATACTTAAAATATCTCTAAAAT
AGGTAAATGTATTTAATTCCATATTGATGAAGATGTTTATTGGTATATTTTCTTTTTCGTCC
TTATATACATATGTAACAGTCAAATATCATTTACTCTTCTTCATTAGCTTTGGGTGCCTTTG
CCACAAGACCTAGCCTAATTTACCAAGGATGAATTCTTTCAATTCTTCATGCGTGCCCTTTT
CATATACTTATTTTATTTTTTACCATAATCTTATAGCACTTGCATCGTTATTAAGCCCTTAT
TTGTTTTGTGTTTCATTGGTCTCTATCTCCTGAATCTAACACATTTCATAGCCTACATTTTA
GTTTCTAAAGCCAAGAAGAATTTATTACAAATCAGAACTTTGGAGGCAAATCTTTCTGCATG
ACCAAAGTGATAAATTCCTGTTGACCTTCCCACACAATCCCTGTACTCTGACCCATAGCACT
CTTGTTTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT
AACACAACTTTATTGATTGAATTTTTAAGCTACTTATTCATAGTTTTATATCCCCCTAAACT
ACCTTTTTGTTCCCCATTCCTTAATTGTATTGTTTTCCCAAGTGTAATTATCATGCGTTTTA
TATCTTCCTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA
ATCTGGTGACAAATATTCTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTCTACCTCTTTT
TTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAGAAGAGGTAGTGTGAATATTAA
TTAGTTTATATTACTCTTATTCTTTGAACATGAACTATGCCTATGTAGTGTCTTTATTTGCT
CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCATGTGATT
CACTGCCTTCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACACACATACCTTCAT
GTGGTTCAGTGCCTTCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACGCACATAC
CTTCATGTGGCTCAGTGCCTTCCTCTCTCTACCAGTCTATTTCCATTCTTTCAGCTGTGTCT
GACATGTTTGTGCTCTGTTCCATTTTAACAACTGCTCTTACTTTTCCAGTCTGTACAGAATG
CTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTTGGCACTGGTGTCTGGAGACCTG
GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGAGCAAGGCATTTGGCTGCTGTAA
GCTTATTGCTTCATCTGTAAGCGGTGGTTTGTAATTCCTGATCTTCCCACCTCACAGTGATG
TTGTGGGGATCCAGTGAGATAGAATACATGTAAGTGTGGTTTTGTAATTTAAAAAGTGCTAT
ACTAAGGGAAAGAATTGAGGAATTAACTGCATACGTTTTGGTGTTGCTTTTCAAATGTTTGA
AAATAAAAAAAATGTTAAG

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185
><subunit 1 of 1, 211 aa, 1 stop
><MW: 22744, pI: 8.51, NX(S/T): 1
MANAGLQLLGFILAFLGWIGAIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCVSQSTGQI
QCKVFDSLLNLSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDDEVQKMRMAVIGGA
IFLLAGLAILVATAWYGNRIVQEFYDPMTPVNARYEFGQALFTGWAAASLCLLGGALLCCSC
PRKTTSYPTPRPYPKPAPSSGKDYV

Important features:
Signal peptide:
amino acids 1-21

Transmembrane domains:
amino acids 82-102, 118-142 and 161-187

N-glycosylation site.
amino acids 72-75

PMP-22 / EMP / MP20 family proteins
amino acids 70-111

ABC-2 type transport system integral membrane protein
amino acids 119-133

FIGURE 99

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG
TGACCGCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTCGCAGAGCACCGGGCAG
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA
AGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGC
GCGATATTTCTTCTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAN
CNTTCAACANTTCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCA
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCT
GTTCCTGTCCC

FIGURE 100

ACCCTTGACCCAACGCGGCCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG
GCTTCATTCTCCCCTTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCCAGGCCNTGTACGAGGGGCTGT
GGATGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGAAGACGATGA
GGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAGGTCTGGCTA
TTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

FIGURE 101

GGGCCCGACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTCGCAGANCACCGGGCAGATCCAGTGCAA
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTT
CTTGCAGGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT
TCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCCTGCGA

FIGURE 102

ATTCTCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT
GCNTGTCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCCAGAAG
ATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC
CACAGCATGGTATGGCAATAGANTNNTTCNNGNNNTCTATGACCCTATGACCCCAGTCAATG
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTG
GGAGGTGCCCTACTTTGCTGTTCCTGTCCC

FIGURE 103

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC
AAGCAACCCCTTGCCTTGAAGGTGGTTGNCATCCCCCCTGGGAGTGAATAGCAATCTTTGTG
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAGGTCTGGCTATTTTAGTNNCCACAGCAT
GGTATGGCAATAGNATNNTTCGNGGNTTCTATGACCCTATGACCCCAGTCAATGCCAGGTAC
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGC
CCTACTTTGCTGTTCCTGTCCCCGAA

FIGURE 104

AGCAATGCCCTGCCCCCAGTGGAGGATTAATTCCTATGNTGGGGACAACATTGTGACNGCCC
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGC
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGTATGA
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTT
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATNGTTCAAGA
ATTTTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG
GCTGGGCTGCTGCTTNTTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTTCCTGCGAACC

FIGURE 105

TCATAGGGGGGCGCGATATTTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA
TGGCAATAGAATCGTTCAAGAATTNTATGACCCTATGACCCCAGTCAATGCCAGGTACGAAT
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA
CTTTGCTGTTCCTG

FIGURE 106

TTCCTGGGATGGATCCGCCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC
TGGCGAACAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT
TGCAAGCAACCNTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAGGTCTGGCTATTTTAGNNGCCACAGCAT
GGTATGGCAATCAGACCCNNTCANAAACTCTATGACCCTATGACCCCAGTCAATGCCAGGTA
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG
CCCTACTTTGCTGTTCCTGTCCCCGAAAAACAACCTCTTACCCACG

FIGURE 107

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGCGCCATCGTCAGCA
CTGCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA
TGTACGAGGGGCTGTGGATGTCNGCGTGTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCT
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNTGCCTTGATGGTGGTTGGCA
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTG
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGC
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT
GACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC
TGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCCTGCGAA

FIGURE 108

GCGTGCCGTCAGCTCGCCGGGCACCGCGGCCTCGCCCTCGCCCTCCGCCCCTGCGCCTGCAC
CGCGTAGACCGACCCCCCCCTCCAGCGCGCCCACCCGGTAGAGGACCCCCGCCCGTGCCCCG
ACCGGTCCCCGCCTTTTTGTAAAACTTAAAGCGGGCGCAGCATTAACGCTTCCCGCCCCGGT
GACCTCTCAGGGGTCTCCCCGCCAAAGGTGCTCCGCCGCTAAGGAACATGGCGAAGGTGGAG
CAGGTCCTGAGCCTCGAGCCGCAGCACGAGCTCAAATTCCGAGGTCCCTTCACCGATGTTGT
CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTAAGGTGAAGACTA
CAGCACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCCTCAATT
AATGTATCTGTGATGTTACAGCCTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT
TATGGTTCAGTCTATGTTTGCTCCAACTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG
CAAAACCGGAAGACCTTATGGATTCAAAACTTAGATGTGTGTTTGAATTGCCAGCAGAGAAT
GATAAACCACATGATGTAGAAATAAATAAAATTATATCCACAACTGCATCAAAGACAGAAAC
ACCAATAGTGTCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG
AAGAATGTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGAACAAGCAGTTCAAG
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTCAGCATTAGC
CCCAACTGGGAAGGAAGAAGGCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTTGTTCTTTA
TCGTTGGTGTAATTATTGGGAAGATTGCCTTGTAGAGGTAGCATGCACAGGATGGTAAATTG
GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGAAATT
AATGTATGATGACATCTCACAGGTCTTGCCTTTAAATTACCCCTCCCTGCACACACATACAC
AGATACACACACACAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG
ATTGAGGGGGAAAAAGAATGATCTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAAT
GGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGCTGGATTACCTC
TCTTAAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCCAGCAT
GCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTG
CTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA
AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT
TGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAA
GCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACTGTTATTCAGAGATGTTTAATGCATA
TTTAACTTATTTAATGTATTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGC
TGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT
GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTATTGGGATGCTGGAGAAGAGCTGCCA
GGAAGTGTTTTTTCTGGGTCAGTAAATAACAACTGTCATAGGGAGGGAAATTCTCAGTAGTG
ACAGTCAACTCTAGGTTACCTTTTTTAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA
CCACCTCTCAACCATTACTCACACTTCCAGCGCCCAGGTCCAAGTCTGAGCCTGACCTCCCC
TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC
ACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAAACTCTTCAGCGAATCCTTCTAGTAC
TAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTTCTGTTTGA
CTATGTAGCATCTTGAAAAGAAAAATTATAATAAAGCCCCAAAATTAAGAAAA

FIGURE 109

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHELKFRGPFTDVVTTNLKLGNPTDRNVCFKVKTTAPRRYCVRPNSGIID
AGASINVSVMLQPFDYDPNEKSKHKFMVQSMFAPTDTSDMEAVWKEAKPEDLMDSKLRCVFE
LPAENDKPHDVEINKIISTTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE
NKQFKEEDGLRMRKTVQSNSPISALAPTGKEEGLSTRLLALVVLFFIVGVIIGKIAL

Important features:

Putative transmembrane domain:

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCCACCTTTCAACCANTACTCACATTTCNAGCGCCCAG
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAAGCC
CCAAAATTAAGAATTCTTTTGTCATTTTGTCACATTTGCTCTATGGGGGGAATTATTATTTT
ATCATTTTTATTATTTTGCCATTGGAAGGTTAACTTTAAAATGAGC

FIGURE 111

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT
AAATGACACCNTTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTGCTTT
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT
AAATTGTATTGGTTCATGTAGTGAAGTCAAACTGTTATTCAGAGATGTTTAATGCATATTTA
ACTTATTTAATGTATTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG
TGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

FIGURE 112

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATTNTTGGGAAGATTGCTTGTAGAGGTA
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG
AAAGTTAAAAATGTATAGTAAC

FIGURE 113

GGTGGCCCATTCCCGGCCCAGGCTGCTTTCCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC
TTGTNATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT
GCTTTGTTCANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACTG
TTATTCAGAGATGTTTAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACTGGTATTGC
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

FIGURE 114

TGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACTGTTATTCAGAGATGTTTAATGC
ATATTTAACTTATTTAATGTATTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA
TGCTGCGTGC

FIGURE 115

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAAACCNTGNGT
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC
TGGATTACCTCTCTTAAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCCANTCCC
GGCCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA
ACAGAGTCAGAAGCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCANTT
AAAGGGNCCAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTTATTCAGAGATG
TTTAATGCATATTTAANTTATTTAATGTATTTCATNTCATGTTTTCTTATTGTCACAAGGGT
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

FIGURE 116

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC
CACGTGGCCCACTCCCGGCCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGC
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACG
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAA
CTGTTATTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTCATCTCATGTTTTC
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTAT
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

FIGURE 117

GCGAGCTCCGGGTGCTGTGGCCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGA
GGCTCCCAGCTGCAGCGTCCCCGCCCGCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC
CTCGGGGACCAAACAAGCCTGGCAGGGTCTCACTTTGTTGCCCAGGCTGGAGTTCAGTGCCA
TGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAAGCGATCCTGCTGAGTAGCTGGGA
CTACAGGACAAAATTAGAAGATCAAAATGGAAAATATGCTGCTTTGGTTGATATTTTTCACC
CCTGGGTGGACCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA
GGTACCCCGGATTGTCAGTGAAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATG
CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCCAGC
CTTTCTGAATTGGAGGATTATCTTTCCTATGAGACTGTCTTTGAGAATGGCACCCGAACCTT
AACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG
TATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTCAGCATCTTGGACAAA
AGGTTCTTAACCAATTTCCCTTTCAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT
TCTCATTTCCCCTCAGCATGTTCTAACTGCTGCCCACTGTGTTCATGATGGAAAGGACTATG
TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG
AAACGTCGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACCAAAGAGAGGGTAC
CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGAGAAGAAGAAAAAAATCTGGCCGGGGTC
AGAGGATTGCCGAAGGGAGGCCTTCCTTTCAGTGGACCCGGGTCAAGAATACCCACATTCCG
AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA
GCTGAAGCGTGCTCACAAAAAGAAATACATGGAACTTGGAATCAGCCCAACGATCAAGAAAA
TGCCTGGTGGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT
CGGTTTTGCAGTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTC
GGGCTCCACCGGTTCGGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAAGAATTGGAAGC
GCAAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTCAGAAGGAC
TACAACGTTGCTGTTCGCATCACTCCCCTAAAATACGCCCAGATTTGCCTCTGGATTCACGG
GAACGATGCCAATTGTGCTTACGGCTAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAA
TCACAGAGAAAACCAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTT
GAACTCTGTCAATAGCATTTCAACATTTTTCAAAATCAGGAGATTTTCGTCCATTTAAAAAA
TGTATAGGTGCAGATATTGAAACTAGGTGGGCACTTCAATGCCAAGTATATACTCTTCTTTA
CATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTTGCCTTCTTAAAAATTAGACACACTTT
AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC
TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAA
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA
CTCTGAGATGGATCCATTCAGCTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT
GGGACATTTAGTTTAGTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGCATTATAAA
CAAAACTAATAACTGTTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAA
TGGGAGAAATAGTTTGTTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTT
TAAGATCTCAAGTTTTTATTTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGG
AAGACACTTCACAAATTATGAATGATCATGTGTTGAAAGCCACATTATTTTATGCTATACAT
TCTATGTATGAGGTGCTACATTTTTAGGACAAAGAATTCTGTAATCTTTTTCAAGAAAGAGT
CTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCTCTGATTAG
TAATTTTAGATATGTCCTTTCCTAAAAATGAATAAAATTTATGAATATGA

FIGURE 118

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFEADAKMMVNTVC
GIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV
YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISPQHVLTAAHCVHDGKDYVKGSKKLRV
GLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGGRRRKKSGRGQRIAEGRPS
FQWTRVKNTHIPKGWARGGMGDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS
GFDNDRADQLVYRFCSVSDESNDLLYQYCDAESGSTGSGVYLRLKDPDKKNWKRKIIAVYSG
HQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGCAAGG
ATCCAAGCATGGAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCTCCTACTCTCTGAGGCGCT
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC
TGCCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA
AGTGCCAAGCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACT
GTGGTTGCACTTCCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAAGGTCCTGATCACTT
ATATCTGGAAACCAAAACCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA
ATGGCTGGACCACTCACAGCAGATTTCATTGTCAAGATTCGTAACTCGGGCTCCGCTGACAG
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC
CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC
CTTATGACCTCTACCATCCCCTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCC
TCGTGTGGGGGGGGCATCCAGAGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCA
TGTCACTTCAGTGGAAGAGTGGAAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT
GGCCAGGGCCTCAGATACCGTGTGGTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGG
CTGTAGCCCAAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA
AACCCAAAGAGAAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA
GAAGAAGGAGCTGCTGTGTCAGAGGAGCCCTCGTAAGTTGTAAAAGCACAGACTGTTCTATA
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA
ACTAAGTGTAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA
AAAAAAAAA

FIGURE 120

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847
<subunit 1 of 1, 525 aa, 1 stop
<MW: 58416, pI: 6.62, NX(S/T): 1
MECCRRATPGTLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTCGGGASYSLRRCLS
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNPCSLKCQ
AKGTTLVVELAPKVLDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVLKGPDHLYLETKTLQGTKGENSLSSTGTFL
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFPCS
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPCTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKLPVEAKLPWFKQAQELEEGAAVSEEPS

Important features:
Signal peptide:
amino acids 1-25

N-glycosylation site.
amino acids 251-254

Thrombospondin 1
amino acids 385-399

von Willebrand factor type C domain proteins
amino acids 385-399, 445-459 and 42-56

FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCCGGTGGGCCCTCGGGCCTGAC
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG
GCCCGCCGGTTCGTGGGGCCCAGGGTCCAGCGGCTGCGCAGAGGCGGGGACCCCGGCCTCAT
GCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGGCCTGGGCCGCGCCACGGCCGCCG
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCGCCGAGGAG
GCGGCGGGTCAGCTCCGCCGCGAGCTCCGCCAGGCCGCGGAGTGCGGCCCAGAGCCTGGCGT
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA
TCTGGGGCACTTTCTACTCACCAATCTTCTCCTTGGACTCCTCAAAAGTTCAGCTCCCAGCA
GGATTGTGGTAGTTTCTTCCAAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC
AGTGAACAAAGCTATAATAAAAGCTTTTGTTATAGCCGGAGCAAACTGGCTAACATTCTTTT
TACCAGGGAACTAGCCCGCCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCCTG
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC
AATTTGGTGTCATGGGCTTTTTCAAAACTCCAGTAGAAGGTGCCCAGACTTCCATTTATTT
GGCCTCTTCACCTGAGGTAGAAGGAGTGTCAGGAAGATACTTTGGGGATTGTAAAGAGGAAG
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACTCTGGGATATCAGTGAAGTG
ATGGTTGGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAAACTGCATATCAG
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACTTGAAGAAAAAGAATTTTG
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTT
TGGGATAAGAGAATTTCAGCAAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATAA
GTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCAAGCATGGATGACATATTA
ATATTTGTCAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT
TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTTTGTGTGGAAATTATCTGC
CTGGTGTGTGCACACAAGTCTTACTTGGAATAAATTTACTGGTAC

FIGURE 122

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747
<subunit 1 of 1, 336 aa, 1 stop
<MW: 36865, pI: 9.15, NX(S/T): 2
MAVATAAAVLAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE
LLRLGARVIMGCRDRARAEEAAGQLRRELRQAAECGPEPGVSGVGELIVRELDLASLRSVRA
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNHLGHFLLTNLLLGLLKSSAPSR
IVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSKLANILFTRELARRLEGTNVTVNVLHPG
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE
LLPKAMDESVARKLWDISEVMVGLLK

Important features:
Signal peptide:
amino acids 1-21

Short-chain alcohol dehydrogenase family protein
amino acids 134-144, 44-56 and 239-248

N-glycosylation site.
amino acids 212-215 and 239-242

FIGURE 123

GGGGATTGTAAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT
TATAAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG
TTACTGAAAAATTATTTTTGGGATAAGAGAATTTCAGCAAAGATGTTTTAAATATATATAGT
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCA
AGCATGGATGACATATTAATATTTGTCAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT
TGTGTGGAAATTATCTGCCTGGCTT

FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCC
CTTTCCTAACCCAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGAC
CCCAGCGTTACC<u>ATG</u>CATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCT
GCTCCTGGTAACTTGGGTTTTTACTCCTGTAACAACTGAAATAACAAGTCTTGCTACAGAGA
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGT
CGTTTCAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCATTAAGGAAGAATT
TCCAAATGAAAATCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC
AGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAG
AGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAG
TGACCCCATTCAAGAAATTCGGGACTTAGCAGAAATCACCACTCTTGATCGCAGCAAAAGAA
ATATCATTGGATATTTTGAGCAAAAGGACTCGGACAACTATAGAGTTTTTGAACGAGTAGCG
AATATTTTGCATGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAAACCGGAAAG
ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACT
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCCTCTT
GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCCAGAATGAAGTAGCTCGGC
AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT
CCTCTTCTGCACATACAGAAAACTCCAGCAGATTGTCCTGTAATCGCTATTGACAGCTTTAG
GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCCTGGAAAACTCAAGCAATTCG
TATTTGACTTACATTCTGGAAAACTGCACAGAGAATTCCATCATGGACCTGACCCAACTGAT
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTT<u>TAA</u>AAACTTG
AAAAACAGTTTGTAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTA
TATTTTCATAATTCTATGTGTATTTTTATTTTGAATAAACAGAAAGAAATTTAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 125

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46927, pI: 5.21, NX(S/T): 0

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQ
MLHPIFEEASDVIKEEFPNENQVVFARVDCDQHSDIAQRYRISKYPTLKLFRNGMMMKREYR
GQRSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKDSDNYRVFERVANILH
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREI
TFENGEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH
IQKTPADCPVIAIDSFRHMYVFGDFKDVLIPGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

FIGURE 126

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATG
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

FIGURE 127

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTCGCCGCNGGAGCCCGGGTCGAGAGGACNAGG
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCCCTTTCCTAACCC
AACCCAACCTAGCCCNGTCCCAGCCGCCAGCGCCTGTCCCTGTCNCGGANCCCAGCGTNACC
ATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC
TTGGGTTTTTACTCCTGTAACAACTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTATGCTGACTGGTGTCGTTTCAGTCAG
ATGTGGCATCCAATTTTTGAGGANGCTTCCGATGTCATTAAGGAAGAATTTCCAAATGAAAA
TCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA
TAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

FIGURE 128

GCCCACGCGTCCG<u>ATG</u>GCGTTCACGTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTTGATGAGCTGAAGACTGAT
TACAAGAATCCTATAGACCAGTGTAATACCCTGAATCCCCTTGTACTCCCAGAGTACCTCAT
CCACGCTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA
TGCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGA
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATG
GTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATGTTT
TGGTGAGCTCT<u>TAG</u>AACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTGCTTGTGGAAAGACTG
TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT
GATTACCTCTGGTGTTGACAGGTTTGAACTTGCACTTCTTAAGGAACAGCCATAATCCTCTG
AATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTTTATAGGAACTTGTA
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAAACTTCATGGGTTTCCTCATCTGTC
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTT
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTT
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAG
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG
TACTACAGATTTTCAAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCTTTAGT
GCAATACAATAAAACTCTGAAATTAAGACTC

FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLA
FYLLAFFYYLYGMIYVLVSS

Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

FIGURE 130

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCTG
AATCCCCTTGTACTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGC
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCTCTTGGCATATCATATTTGGAGGTATA
TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTT
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACAACACACAGAAGAATT
GGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

FIGURE 131

CGGACGCGTGGGGGAAACCCTTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG
GAACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGC
TGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTCGGGGACCGCTTCGGCTGAAGCATTTGAC
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCACAC
CTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTC
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA
GAAGCATATTCGCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC
ATTCGCTGAACTGAGACAAGAACAACTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC
TCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCC
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA
GCAAAATGTCCTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGA
GAAAGTGATGGCTTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACTCT
TGTCCTCTCGGTGATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGC
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG
CTAAACAGATATCCAGCTTCTTCTCTTGTGGTTGTTAGATCTAAAACTGAAGATCATGAAGA
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTT
AAAAGACAAGTGTAATAGACATCTAAAATTCCACTCCTCATAGAGCTTTTAAAATGGTTTCA
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847
<subunit 1 of 1, 323 aa, 1 stop
<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGSLWVRTQLGLPPLLLLTMALAGGSGTASAEAFDSVLGDTASCHRACQLTYPLHTYP
KEEELYACQRGCRLFSICQFVDDGIDLNRTKLECESACTEAYSQSDEQYACHLGCQNQLPFA
ELRQEQLMSLMPKMHLLFPLTLVRSFWSDMMDSAQSFITSSWTFYLQADDGKIVIFQSKPEI
QYAPHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVL
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG
PLPTKVNLAHSEI

Important features:

Signal peptide:
amino acids 1-31

Transmembrane domain:
amino acids 241-260

N-glycosylation site.
amino acids 90-93

FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCACACCTACCC
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTCGC
TGAACTGAGACAAGAACAACTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAA
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

FIGURE 134

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC
CCAACTGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTCGGGGACCG
CTTCGGCTGAAGCATTTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG
TTGACCTACCCCTTGCACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG
AATGTGAATCTGCATGTACAGAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTT
GGTTGCCAGAATCAGCTGCCATTCGCTGAACTGAGACAAGAACAACTTATGTCCCTGATGCC
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT
CCGC

FIGURE 135

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCGGAGGT
GGGGCGCCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGCGACCGAGC
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCAATGGGCCGCGGCTG
GGGATTCTTGTTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC
AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT
ACCTGTGATGTTGAAACCATTGATAGATTTAATAACTACAGGCTTTTCCCAAGACTACAAAA
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCCTTTCT
GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA
GTTCCTGATGGAATTAAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC
ATTCAGTCCCCTGAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA
CAAGGGACCAGATGCTTGGAAAATATGGAATGTCATCTACGAAGAAAACTGTTTTAAGCCAC
AGACAATTAAAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACACT
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATATCTGG
CCTACATGCAAGCATTAATGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAG
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTTGATGGAATTTTGACTGAA
GGAGAAGGTCCAAGAAGGCTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTT
ATCCAAAGTGTTACCATTCTTCGAGCGCCCAGATTTTCAACTCTTTACTGGAAATAAAATTC
AGGATGAGGAAAACAAAATGTTACTTCTGGAAATACTTCATGAAATCAAGTCATTTCCTTTG
CATTTTGATGAGAATTCATTTTTTGCTGGGGATAAAAAAGAAGCACACAAACTAAAGGAGGA
CTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC
GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG
AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATTCCATCTAACCAGACAAGA
AATAGTATCATTATTCAACGCATTTGGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAACT
TCAGGAACTTGTTACAGAATATTCATTAAAGAAAACAAGCTGATATGTGCCTGTTTCTGGAC
AATGGAGGCGAAAGAGTGGAATTTCATTCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA
ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTGTTTTAAGTAAACACATTTTT
AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAAGTAATACTTTAATAATGTG
GTACAAATTTTAAAGTTTAATATTGAATAAAAGGAGGATTATCAAATTAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 136

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974
<subunit 1 of 1, 468 aa, 1 stop
<MW: 54393, pI: 5.63, NX(S/T): 2

MGRGWGFLFGLLGAVWLLSSGHGEEQPPETAAQRCFCQVSGYLDDCTCDVETIDRFNNYRLF
PRLQKLLESDYFRYYKVNLKRPCPFWNDISQCGRRDCAVKPCQSDEVPDGIKSASYKYSEEA
NNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLLNPE
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAFY
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI
ELRALSKVLPFFERPDFQLFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH
KLKEDFRLHFRNISRIMDCVGCFKCRLWGKLQTQGLGTALKILFSEKLIANMPESGPSYEFH
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

Important features:

Signal peptide:
amino acids 1-23

N-glycosylation site.
amino acids 280-283 and 384-387

Amidation site.
amino acids 94-97

Glycosaminoglycan attachment site.
amino acids 20-23 and 223-226

Aminotransferases class-V pyridoxal-phosphate
amino acids 216-222

Interleukin-7 proteins
amino acids 338-343

FIGURE 137

GCTGGAAATATGGATGTCATCTACGAGAAACTGTTTTAAGCCACAGACAATTAAAAGACCTT
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA
GGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA
ACATTACAGAATTTNAACAGCGATTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG
CTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT
CTTNGAGCGCCCAGATTTTCAACTNTTTACTGGAAATAAAATTCAGGATGAGGNAAACAAAA
TGTTACTTTTGGAAATACTTCATGAAATCAAGTCATTTCCTTTGCATTTTGATGAGAATTCA
TTTTTTTGCTG

FIGURE 138

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGGAGGGGGCAGGATGGGAGGGAA
AGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC
CGATCAGGC<u>ATG</u>GAACTCCCCTTCGTCACTCACCTGTTCTTGCCCCTGGTGTTCCTGACAGG
TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTCCCAGGGCCACCAGAAG
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC
GCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG
GGCCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTC
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTC
ATGGTGAGC<u>TAA</u>GGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAAGAGAA
GTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCCTAGAAAGCAAA
AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT
GCCCTCCCAAGCCTGGGAGTAACTATTTCCCCCATCCCCAGGCCTGTGCCCCTCTCTGGTCT
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCA
GCCTCAGGGAAGCCTGGCACCCACTGCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTT
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCTGGCAAAGGG
CCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAAGCTCCATGTTTCCTAACAGA
TTCAGACTCCTGGCCAGGTGTGGTGGCCCACACCTGTAATTCTAGCACTTTGGGAGGCCAAG
GTGGGCAGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACTCCAT
CTCTACTAAAAAAAAAAAAATACAAAAATTAGCTGGGTGCGCTAGTGCATGCCTGTAATCTC
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG
AGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA
AATAATAATAATAATAATTCAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

FIGURE 139

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039

><subunit 1 of 1, 124 aa, 1 stop

><MW: 13352, pI: 5.99, NX(S/T): 1

MELPFVTHLFLPLVFLTGLCSPFNLDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW
DGPSGDRRGDVYRCPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETDGDGGFMVS

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

FIGURE 140

CACAGTTCCCCACCATCACTCNTCCCATTCCTTCCAACTTTATTTTTAGCTTGCCATTGGGA
GGGGGCAGGATGGGAGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC
TTCTCATACTGGACAGAAACCGATCAGGCATGGAACTCCCCTTCGTCACTCACCTGTTCTTG
CCCCTGGTGTTCCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT
ATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT
TATCGCTGCCCTGTAGGGGGGGCCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTA
CCAACTGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA
CAGATGGTGATGG

FIGURE 141

AAAGTTACATTTTCTCTGGAACTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA
ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
GAGATGGACAGAATGCTTTATTTGGAAAGAAACAATGTTCTAGGTCAAACTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCCTCAGAACCTC
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGA
AACAGTGTACTATTCTGTCGAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATC
ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTG
GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG
GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCTTTGTTGGCTTCATGCTGATCCTTGT
GGTCGTGCCACTGTTCGTCTGGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG
TGGTCCTCCCAGACACCTTGAAAATAACCAATTCACCCCAGAAGTTAATCAGCTGCAGAAGG
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGAT
CTCATAGGTTTGCGGAAGGGCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC
CTGGGAAAAGTGACTTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC
TACACACCTGCTAAACACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA
TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTCAG
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
GGCTTGGAGAGCCCACTTTCCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
TGTTGAGTTCACTTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
AGGTGACCTGGAGGAAGGTCACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
CATGAACTACTGTAAAGTGTTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTTGTGCTCCTTTTTTC
TGTTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA
AAAAAAAAAA

FIGURE 142

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033
<subunit 1 of 1, 311 aa, 1 stop
<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLLMWSPVIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTSAW
SILKHPFNRNSTILTRPGMEITKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLVLALFAFVGFMLILV
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:
amino acids 1-29

Transmembrane domain:
amino acids 230-255

N-glycosylation site.
amino acids 40-43 and 134-137

Tissue factor proteins.
amino acids 92-119

Integrins alpha chain proteins
amino acids 232-262

FIGURE 143

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTCGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 144

CCCACGCGTCCGCCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA
GGCAGGAGAGGAGGAGGTGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGG
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG
GCTGCTTTGGCATTTGGGGAACTGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT
GGAGGGACAGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGCAGGGCGTTGGG
CAGGGGTCCCTCGGAGGCCTCCTGGGG<u>ATG</u>GGGGCTGCAGCTCGTCTGAGCGCCCCTCGAGC
GCTGGTACTCTGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAAACTTCGTGCCAGGGCCTCCTTTCTGGGGC
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCCATTAAGGCTCAGCACTGGAGGAGAGA
AGCTCCGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCT
GTGGTCAATGTGTCTGGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAACTGCGGCTGCT
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTG
AGGTGCAGCTCATTCACTTCAACCAGGAACTCTACGGGAATTTCAGCGCTGCCTCCCGCGGC
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCATTCCT
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTC
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC
TCTCTCAGCACCCCGCCCTGCTCCGAGACTGTCACCTGGATCCTCATTGACCGGGCCCTCAA
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT
TCCAGAGCCTCAGCGGTAACAGCCGGCCCCTGCAGCCCTTGGCCCACAGGGCACTGAGGGGC
AACAGGGACCCCCGGCACCCCGAGAGGCGCTGCCGAGGCCCCAACTACCGCCTGCATGTGGA
TGGTGTCCCCCATGGTCGC<u>TGA</u>GACTCCCCTTCGAGGATTGCACCCGCCCGTCCTAAGCCTC
CCCACAAGGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTA

FIGURE 145

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353
<subunit 1 of 1, 328 aa, 1 stop
<MW: 36238, pI: 9.90, NX(S/T): 3
MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPL
LYSHRLSELRLLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL
FVNVASTSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE
TVTWILIDRALNITSLQMHSLRLLSQNPPSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER
RCRGPNYRLHVDGVPHGR

Important features:

Signal peptide:
amino acids 1-23

Transmembrane domain:
amino acids 177-199

N-glycosylation site.
amino acids 118-121, 170-173 and 260-263

Eukaryotic-type carbonic anhydrases proteins
amino acids 222-270, 128-164 and 45-92

FIGURE 146

GGCGCCTGGTTCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTCGCCGCCAGCCTCC
GCCGCCGAGCCTCGTTCGTGTCCCCGCCCCTCGCTCCTGCAGCTACTGCTCAGAAACGCTGG
GGCGCCCACCCTGGCAGACTAACGAAGCAGCTCCCTTCCCACCCCAACTGCAGGTCTAATTT
TGGACGCTTTGCCTGCCATTTCTTCCAGGTTGAGGGAGCCGCAGAGGCGGAGGCTCGCGTAT
TCCTGCAGTCAGCACCCACGTCGCCCCCGGACGCTCGGTGCTCAGGCCCTTCGCGAGCGGGG
CTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCCGGCCGTCCGGTTTG
GCTCACCTCTCCCAGGAAACTTCACACTGGAGAGCCAAAAGGAGTGGAAGAGCCTGTCTTGG
AGATTTTCCTGGGGAAATCCTGAGGTCATTCATTATGAAGTGTACCGCGCGGGAGTGGCTCA
GAGTAACCACAGTGCTGTTCATGGCTAGAGCAATTCCAGCCATGGTGGTTCCCAATGCCACT
TTATTGGAGAAACTTTTGGAAAAATACATGGATGAGGATGGTGAGTGGTGGATAGCCAAACA
ACGAGGGAAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCATAATAAAT
TACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTG
GAAAGATCTGCAGAATCCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGCT
TCCATCAATTGGACAGAATTTGGGAGCACACTGGGGAAGATATAGGCCCCCGACGTTTCATG
TACAATCGTGGTATGATGAAGTGAAAGACTTTAGCTACCCATATGAACATGAATGCAACCCA
TATTGTCCATTCAGGTGTTCTGGCCCTGTATGTACACATTATACACAGGTCGTGTGGGCAAC
TAGTAACAGAATCGGTTGTGCCATTAATTTGTGTCATAACATGAACATCTGGGGGCAGATAT
GGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAAGGGAAACTGGTGGGCCATGCC
CCTTACAAACATGGGCGGCCCTGTTCTGCTTGCCCACCTAGTTTTGGAGGGGGCTGTAGAGA
AAATCTGTGCTACAAAGAAGGGTCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATG
AAATAGAACGACAGCAGTCACAAGTCCATGACACCCATGTCCGGACAAGATCAGATGATAGT
AGCAGAAATGAAGTCATAAGCGCACAGCAAATGTCCCAAATTGTTTCTTGTGAAGTAAGATT
AAGAGATCAGTGCAAAGGAACAACCTGCAATAGGTACGAATGTCCTGCTGGCTGTTTGGATA
GTAAAGCTAAAGTTATTGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCA
ATTCATTATGGTATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAA
GCATTATTTCATCAAGTCCAATAGAAATGGTATTCAAACAATTGGCAAATATCAGTCTGCTA
ATTCCTTCACAGTCTCTAAAGTAACAGTTCAGGCTGTGACTTGTGAAACAACTGTGGAACAG
CTCTGTCCATTTCATAAGCCTGCTTCACATTGCCCAAGAGTATACTGTCCTCGTAACTGTAT
GCAAGCAAATCCACATTATGCTCGTGTAATTGGAACTCGAGTTTATTCTGATCTGTCCAGTA
TCTGCAGAGCAGCAGTACATGCTGGAGTGGTTCGAAATCACGGTGGTTATGTTGATGTAATG
CCTGTGGACAAAAGAAAGACCTACATTGCTTCTTTTCAGAATGGAATCTTCTCAGAAAGTTT
ACAGAATCCTCCAGGAGGAAAGGCATTCAGAGTGTTTGCTGTTGTGTGAAACTGAATACTTG
GAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGAATTTTGTATAAAACTGTAACA
TTACTGTACAGAGTACATCAACTATTTTCAGCCCAAAAAGGTGCCAAATGCATATAAATCTT
GATAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAATAT
AATGGTTTTAGAAATCCTGTGTTAAATATTGCTATATTTTCTTAGCAGTTATTTCTACAGTT
AATTACATAGTCATGATTGTTCTACGTTTCATATATTATATGGTGCTTTGTATATGCCACTA
ATAAAATGAATCTAAACATTGAATGTGAATGGCCCTCAGAAAATCATCTAGTGCATTTAAAA
ATAATCGACTCTAAAACTGAAAGAAACCTTATCACATTTCCCCAGTTCAATGCTATGCCAT
TACCAACTCCAAATAATCTCAAATAATTTCCACTTAATAACTGTAAAGTTTTTTTCTGTTA
ATTTAGGCATATAGAATATTAAATTCTGATATTGCACTTCTTATTTTATATAAAATAATCCT
TTAATATCCAAATGAATCTGTTAAAATGTTTGATTCCTTGGGAATGGCCTTAAAAATAAATG
TAATAAAGTCAGAGTGGTGGTATGAAAACATTCCTAGTGATCATGTAGTAAATGTAGGGTTA
AGCATGGACAGCCAGAGCTTTCTATGTACTGTTAAAATTGAGGTCACATATTTTCTTTTGTA
TCCTGGCAAATACTCCTGCAGGCCAGGAAGTATAATAGCAAAAAGTTGAACAAAGATGAACT
AATGTATTACATTACCATTGCCACTGATTTTTTTAAATGGTAAATGACCTTGTATATAAAT
ATTGCCATATCATGGTACCTATAATGGTGATATATTTGTTTCTATGAAAAATGTATTGTGCT
TTGATACTAAAAATCTGTAAAATGTTAGTTTGGTAATTTTTTTCTGCTGGTGGATTTACA
TATTAAATTTTTTCTGCTGGTGGATAAACATTAAAATTAATCATGTTTCAAAAAAAAAAAAA

FIGURE 147

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEDGEWWIAKQRGKRAITDNDM
QSILDLHNKLRSQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW
GRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGCAINLC
HNMNIWGQIWPKAVYLVCNYSPKGNWWGHAPYKHGRPCSACPPSFGGGCRENLCYKEGSDRY
YPPREEETNEIERQQSQVHDTHVRTRSDDSSRNEVISAQQMSQIVSCEVRLRDQCKGTTCNR
YECPAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKHYFIKSNRNGI
QTIGKYQSANSFTVSKVTVQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIG
TRVYSDLSSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNPPGGKAFRV
FAVV

Important features:

Signal peptide:

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

FIGURE 148

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT
GGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCG
CGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGGCGCTGT
ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC
AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT
CATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAAGCTGC
AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGAA
GAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTGTGCAAAGGA
CTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCCTTTC
TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAG
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCT
CCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTTAA
AAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGA
GGAACAATGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGC
TTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT
CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCT
GGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC
CTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATA
TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACT
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA
AACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT
TTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGAT
GACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCC
CAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCAT
TGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAA
AAAAAAAAAAA

FIGURE 149

MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE

FIGURE 150

GCCCCAGGGACTGCTATGGCTTCCTTTGTTGTTCACCCCGGTCTGCGTCATGTTAAACTCCA
ATGTCCTCCTGTGGTTAACTGCTCTTGCCATCAAGTTCACCCTCATTGACAGCCAAGCACAG
TATCCAGTTGTCAACACAAATTATGGCAAAATCCGGGGCCTAAGAACACCGTTACCCAATGA
GATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCCTATGCCTCACCCCCCACTGGAGAGA
GGCGGTTTCAGCCCCCAGAACCCCCGTCCTCCTGGACTGGCATCCGAAATACTACTCAGTTT
GCTGCTGTGTGCCCCCAGCACCTGGATGAGAGATCCTTACTGCATGACATGCTGCCCATCTG
GTTTACCGCCAATTTGGATACTTTGATGACCTATGTTCAAGATCAAAATGAAGACTGCCTTT
ACTTAAACATCTACGTGCCCACGGAAGATGGAGCCAACACAAAGAAAAACGCAGATGATATA
ACGAGTAATGACCGTGGTGAAGACGAAGATATTCATGATCAGAACAGTAAGAAGCCCGTCAT
GGTCTATATCCATGGGGGATCTTACATGGAGGGCACCGGCAACATGATTGACGGCAGCATTT
TGGCAAGCTACGGAAACGTCATCGTGATCACCATTAACTACCGTCTGGGAATACTAGGGTTT
TTAAGTACCGGTGACCAGGCAGCAAAAGGCAACTATGGGCTCCTGGATCAGATTCAAGCACT
GCGGTGGATTGAGGAGAATGTGGGAGCCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTG
GCTCGGGGGCTGGGGCCTCCTGTGTCAGCCTGTTGACCCTGTCCCACTACTCAGAAGGTCTC
TTCCAGAAGGCCATCATTCAGAGCGGCACCGCCCTGTCCAGCTGGGCAGTGAACTACCAGCC
GGCCAAGTACACTCGGATATTGGCAGACAAGGTCGGCTGCAACATGCTGGACACCACGGACA
TGGTAGAATGCCTGCGGAACAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCCGGCC
ACCTACCACATAGCCTTCGGGCCGGTGATCGACGGCGACGTCATCCCAGACGACCCCCAGAT
CCTGATGGAGCAAGGCGAGTTCCTCAACTACGACATCATGCTGGGCGTCAACCAAGGGGAAG
GCCTGAAGTTCGTGGACGGCATCGTGGATAACGAGGACGGTGTGACGCCCAACGACTTTGAC
TTCTCCGTGTCCAACTTCGTGGACAACCTTTACGGCTACCCTGAAGGGAAAGACACTTTGCG
GGAGACTATCAAGTTCATGTACACAGACTGGGCCGATAAGGAAAACCCGGAGACGCGGCGGA
AAACCCTGGTGGCTCTCTTTACTGACCACCAGTGGGTGGCCCCCGCCGTGGCCGCCGACCTG
CACGCGCAGTACGGCTCCCCCACCTACTTCTATGCCTTCTATCATCACTGCCAAAGCGAAAT
GAAGCCCAGCTGGGCAGATTCGGCCCATGGTGATGAGGTCCCCTATGTCTTCGGCATCCCCA
TGATCGGTCCCACCGAGCTCTTCAGTTGTAACTTTTCCAAGAACGACGTCATGCTCAGCGCC
GTGGTCATGACCTACTGGACGAACTTCGCCAAAACTGGTGATCCAAATCAACCAGTTCCTCA
GGATACCAAGTTCATTCACACAAAACCCAACCGCTTTGAAGAAGTGGCCTGGTCCAAGTATA
ATCCCAAAGACCAGCTCTATCTGCATATTGGCTTGAAACCCAGAGTGAGAGATCACTACCGG
GCAACGAAAGTGGCTTTCTGGTTGGAACTCGTTCCTCATTTGCACAACTTGAACGAGATATT
CCAGTATGTTTCAACAACCACAAAGGTTCCTCCACCAGACATGACATCATTTCCCTATGGCA
CCCGGCGATCTCCCGCCAAGATATGGCCAACCACCAAACGCCCAGCAATCACTCCTGCCAAC
AATCCCAAACACTCTAAGGACCCTCACAAAACAGGGCCTGAGGACACAACTGTCCTCATTGA
AACCAAACGAGATTATTCCACCGAATTAAGTGTCACCATTGCCGTCGGGGCGTCGCTCCTCT
TCCTCAACATCTTAGCTTTTGCGGCGCTGTACTACAAAAAGGACAAGAGGCGCCATGAGACT
CACAGGCGCCCCAGTCCCCAGAGAAACACCACAAATGATATCGCTCACATCCAGAACGAAGA
GATCATGTCTCTGCAGATGAAGCAGCTGGAACACGATCACGAGTGTGAGTCGCTGCAGGCAC
ACGACACACTGAGGCTCACCTGCCCGCCAGACTACACCCTCACGCTGCGCCGGTCGCCAGAT
GACATCCCACTTATGACGCCAAACACCATCACCATGATTCCAAACACACTGACGGGGATGCA
GCCTTTGCACACTTTTAACACCTTCAGTGGAGGACAAAACAGTACAAATTTACCCCACGGAC
ATTCCACCACTAGAGTATAGCTTTGCCCTATTTCCCTTCCTATCCCTCTGCCCTACCCGCTC
AGCAACATAGAAGAGGGAAGGAAAGAGAGAAGGAAAGAGAGAGAGAAAGAAAGTCTCCAGAC
CAGGAATGTTTTTGTCCCACTGACTTAAGACAAAAATGCAAAAAGGCAGTCATCCCATCCCG
GCAGACCCTTATCGTTGGTGTTTTCCAGTATTACAAGATCAACTTCTGACCCTGTGAAATGT
GAGAAGTACACATTTCTGTTAAAATAACTGCTTTAAGATCTCTACCACTCCAATCAATGTTT
AGTGTGATAGGACATCACCATTTCAAGGCCCCGGGTGTTTCCAACGTCATGGAAGCAGCTGA
CACTTCTGAAACTCAGCCAAGGACACTTGATATTTTTTAATTACAATGGAAGTTTAAACATT
TCTTTCTGTGCCACACAATGGATGGCTCTCCTTAAGTGAAGAAAGAGTCAATGAGATTTTGC
CCAGCACATGGAGCTGTAATCCAGAGAGAAGGAAACGTAGAAATTTATTATTAAAAGAATGG
ACTGTGCAGCGAAATCTGTACGGTTCTGTGCAAAGAGGTGTTTTGCCAGCCTGAACTATATT
TAAGAGACTTTGT

FIGURE 151

MLNSNVLLWLTALAIKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP
PTGERRFQPPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMLPIWFTANLDTLMTYVQDQN
EDCLYLNIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR
VTIFGSGAGASCVSLLTLSHYSEGLFQKAIIQSGTALSSWAVNYQPAKYTRILADKVGCNML
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLGV
NQGEGLKFVDGIVDNEDGVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIKFMYTDWADKENP
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKPSWADSAHGDEVPYV
FGIPMIGPTELFSCNFSKNDVMLSAVVMTYWTNFAKTGDPNQPVPQDTKFIHTKPNRFEEVA
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPPDMTS
FPYGTRRSPAKIWPTTKRPAITPANNPKHSKDPHKTGPEDTTVLIETKRDYSTELSVTIAVG
ASLLFLNILAFAALYYKKDKRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE
SLQAHDTLRLTCPPDYTLTLRRSPDDIPLMTPNTITMIPNTLTGMQPLHTFNTFSGGQNSTN
LPHGHSTTRV

FIGURE 152

GGGAAAG<u>ATG</u>GCGGCGACTCTGGGACCCCTTGGGTCGTGGCAGCAGTGGCGGCGATGTTTGT
CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTCTTTTGTTGGGGTCTGGGCAGGGGCCA
CAGCAAGTCGGGGCGGGTCAAACGTTCGAGTACTTGAAACGGGAGCACTCGCTGTCGAAGCC
CTACCAGGGTGTGGGCACAGGCAGTTCCTCACTGTGGAATCTGATGGGCAATGCCATGGTGA
TGACCCAGTATATCCGCCTTACCCCAGATATGCAAAGTAAACAGGGTGCCTTGTGGAACCGG
GTGCCATGTTTCCTGAGAGACTGGGAGTTGCAGGTGCACTTCAAAATCCATGGACAAGGAAA
GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC
CTGTGTTTGGAAACATGGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT
GAGGAGAAGCAGCAAGAGCGGGTATTCCCCTACATCTCAGCCATGGTGAACAACGGCTCCCT
CAGCTATGATCATGAGCGGGATGGGCGGCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC
GCAATCTTCATTACGACACCTTCCTGGTGATTCGCTACGTCAAGAGGCATTTGACGATAATG
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCCTGCC
CCGCGGCTACTACTTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA
TTTCCTTGAAGTTGTTTGAACTGACAGTGGAGAGAACCCCAGAAGAGGAAAAGCTCCATCGA
GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC
CCTGAGTGGCCTGGCCCTCTTCCTCATCGTCTTTTTCTCCCTGGTGTTTTCTGTATTTGCCA
TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTAC<u>TGA</u>
GCCCTCCTGCTGCCACCACTTTTGTGACTGTCACCCATGAGGTATGGAAGGAGCAGGCACTG
GCCTGAGCATGCAGCCTGGAGAGTGTTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTG
TCACTGGAGTTTTGAATGCAGGGACCCCGCATTCCCATGGTTGTGCATGGGGACATCTAACT
CTGGTCTGGGAAGCCACCCACCCCAGGGCAATGCTGCTGTGATGTGCCTTTCCCTGCAGTCC
TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGCCAAAATCACAGAAC
AGAATTTCATAGCCCAGGCTGCCGTGTTGTTTGACTCAGAAGGCCCTTCTACTTCAGTTTTG
AATCCACAAAGAATTAAAAACTGGTAACACCACAGGCTTTCTGACCATCCATTCGTTGGGTT
TTGCATTTGACCCAACCCTCTGCCTACCTGAGGAGCTTTCTTTGGAAACCAGGATGGAAACT
TCTTCCCTGCCTTACCTTCCTTTCACTCCATTCATTGTCCTCTCTGTGTGCAACCTGAGCTG
GGAAAGGCATTTGGATGCCTCTCTGTTGGGGCCTGGGGCTGCAGAACACACCTGCGTTTCAC
TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTGTTCCCTAGCAT
GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTG
AAGTTTGGCTAAAGGTTGGTGTAAAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG
GATTAGCTGTGCAACTGACCAGCTCCAGGTTTGATCAAACCAAAAGCAACATTTGTCATGTG
GTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTTTGTAGT
TACGATTTTTGGAATCCCACTTTGAGTGCTGAAAGTGTAAGGAAGCTTTCTTCTTACACCTT
GGGCTTGGATATTGCCCAGAGAAGAAATTTGGCTTTTTTTTTCTTAATGGACAAGAGACAGT
TGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCCTGGAAGAGTT
CACTGTCATTGAGCAGCACAGCCTGAGTGCTGGCCTCTGTCAACCCTTATTCCACTGCCTTA
TTTGACAAGGGGTTACATGCTGCTCACCTTACTGCCCTGGGATTAAATCAGTTACAGGCCAG
AGTCTCCTTGGAGGGCCTGGAACTCTGAGTCCTCCTATGAACCTCTGTAGCCTAAATGAAAT
TCTTAAAATCACCGATGGAACCAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCG
ACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCCATGG

FIGURE 153

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39711, pI: 8.70, NX(S/T): 1

MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPQQVGAGQTFEYLKREHSLSKPYQ
GVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKIHGQGKKN
LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDTYPNEEKQQERVFPYISAMVNNGSLSY
DHERDGRPTELGGCTAIVRNLHYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG
YYFGTSSITGDLSDNHDVISLKLFELTVERTPEEEKLHRDVFLPSVDNMKLPEMTAPLPPLS
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

FIGURE 154

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATC
TACGGATCAGTCTCTGATGGTGGGTCGTTAACCTCAGTGGGGACTCCAAGATTTCCATGAAG
AAAATCAGTTGTCTTCATTCAAGAATTGGGGTCTGGCTCAGAATTCCTGCAGCTGGTGAAAA
TCTGTTTTCTAGAAGAGGTTTAATTAATGCCTGCAGTCTGACATGTTCCCGATTTGAGGTGA
AACCATGAAGAGAAAATAGAATACTTAATAATGCTTTTCCGCAACCGCTTCTTGCTGCTGCT
GGCCCTGGCTGCGCTGCTGGCCTTTGTGAGCCTCAGCCTGCAGTTCTTCCACCTGATCCCGG
TGTCGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAAGAGAATCATGCCCGACCCTGTG
ACGGAGCCCCCTGTGACAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCCAGTGT
GGCCGAGCGCAGCATGGAAGGTCATGCCCCGCATCATTTTAAGCTGGTCTCAGTGCATGTGT
TCATTCGCCACGGAGACAGGTACCCACTGTATGTCATTCCCAAAACAAAGCGACCAGAAATT
GACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAAACTGGAAGCTTTCATTAGTCA
CATGTCAAAAGGATCCGGAGCCTCTTTCGAAAGCCCCTTGAACTCCTTGCCTCTTTACCCAA
ATCACCCATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTGCAGAAC
GGTCAGCTGCTGAGGGATATCTATCTAAAGAAACACAAACTCCTGCCCAATGATTGGTCTGC
AGACCAGCTCTATTTAGAGACCACTGGGAAAAGCCGGACCCTACAAAGTGGGCTGGCCTTGC
TTTATGGCTTTCTCCCAGATTTTGACTGGAAGAAGATTTATTTCAGGCACCAGCCAAGTGCG
CTGTTCTGCTCTGGAAGCTGCTATTGCCCGGTAAGAAACCAGTATCTGGAAAAGGAGCAGCG
TCGTCAGTACCTCCTACGTTTGAAAAACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCA
AGATCGTGGATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGC
CACTTCTGCCACAATGTCAGCTTTCCCTGTACCAGAAATGGCTGTGTTGACATGGAGCACTT
CAAGGTAATTAAGACCCATCAGATCGAGGATGAAAGGGAAAGACGGGAGAAGAAATTGTACT
TCGGGTATTCTCTCCTGGGTGCCCACCCCATCCTGAACCAAACCATCGGCCGGATGCAGCGT
GCCACCGAGGGCAGGAAAGAAGAGCTCTTTGCCCTCTACTCTGCTCATGATGTCACTCTGTC
ACCAGTTCTCAGTGCCTTGGGCCTTTCAGAAGCCAGGTTCCCAAGGTTTGCAGCCAGGTTGA
TCTTTGAGCTTTGGCAAGACAGAGAAAAGCCCAGTGAACATTCCGTCCGGATTCTTTACAAT
GGCGTCGATGTCACATTCCACACCTCTTTCTGCCAAGACCACCACAAGCGTTCTCCCAAGCC
CATGTGCCCGCTTGAAAACTTGGTCCGCTTTGTGAAAAGGGACATGTTTGTAGCCCTGGGTG
GCAGTGGTACAAATTATTATGATGCATGTCACAGGGAAGGATTCTAAAAGGTATGCAGTACA
GCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAAGGTCCACTTCTAGTTTTGTCTGTT
ACTAAGGGTAGAAGATTATTGCTTTTTAAAGGCTAAATATTGTTTGTGGGAACCACAGATGG
TTGGGGTTGAACAGTAAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAAATGG
CCAGTTCACAGAGGAATAGAAGGTACTTTATCATAGCCAGACTTCGCTTAGAATGCCAGAAT
AATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCACTCTTCTGGCCTGCCCCATGTT
ACTATGTGATGGAACCAGCACACCTCAACCAAAATTTTTTAATCTTAGACATTTTTACCTT
GTCCTTGTTAAGAATTTCTTGAAGTGATTTATCTAAAATAAAGGTTGGCAAACTTTTTCTGT
AAAGGGCCAGATTGTAAATATTTCAGACTGTGTGGACCAAAAGGCCACATACAGTCTCTGTC
ATAACTACTCAACTCTGTTTCTGAAGCAGGAAAGCCACCACAGACAGTACATAAAGGAATAT
GTGTAGCTGGGTTCCCAGGCCAGACAAAACAGATGGTGACCAGACTTGGCCCCTGGGCTGTA
GTTTGCTGACCCCTCATCTAAAAAATAGGCTATACTACAATTGCACTTCCAGCACTTTGAGA
ACGAGTTGAATACCAAGAATTATTCAATGGTTCCTCCAGTAACTTCTGCTAGAAACACAGAA
TTTGGTCTGTATCTGACACTAGAACAAAACTTGAGGGTAAATAAACATTGAATTAGAATGAA
TCATAGAAAACTGATTAGAAGAATACTTGATGTTTATGATGATTGTGGTACAAGATAGTTTT
AAGTATGTTCTAAATATTTGTCTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTTGTAT
GCCATTTAGTATTTTTATAGTTTAGGAAAATATTTTCTAAGACCAGTTTTAGATGACTCTTA
TTCCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAGGAGGCTAGAAGATGA
ATTCAGGCACTTTCTTCCAATAAAACTAATTATGGCTCATTCCCTTTGACAAGCTGTAGAAC
TGGATTCATTTTTAAACCATTTTCATCAGTTTCAAATGGTAAATTCTGATTGATTTTTAAAT
GCGTTTTTGGAAGAACTTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATAT
TAGAAGCAATTATAATTACATCTGTGATTTCTGAACTAATGGTGCTAATTCAGAGAAATGGA
AAGTGAAAGTGAGATTCTCTGTTGTCATCGGCATTCCAACTTTTTCTCTTTGTTTTTGTCCA
GTGTTGCATTTGAATATGTCTGTTTCTATAAATAAATTTTTTAAGAATAA

FIGURE 155

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329
><subunit 1 of 1, 480 aa, 1 stop
><MW: 55240, pI: 9.30, NX(S/T): 2

MLFRNRFLLLLALAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDPVTEPPVTDPVY
EALLYCNIPSVAERSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKP
YHPKLEAFISHMSKGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK
KHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMLCHFCHNVSFPC
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELF
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSEHSVRILYNGVDVTFHTSF
CQDHHKRSPKPMCPLENLVRFVKRDMFVALGGSGTNYYDACHREGF

FIGURE 156

AAAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCCATCCCCTTTTGAAGA
ACAGTACTGTGGAGCTATTTAAGAGATAAAAACGAAATATCCTTTCTGGGAGTTCAAGATTG
TGCAGTAATTGGTTAGGACTCTGAGCGCCGCTGTTCACCAATCGGGGAGAGAAAAGCGGAGA
TCCTGCTCGCCTTGCACGCGCCTGAAGCACAAAGCAGATAGCTAGGAATGAACCATCCCTGG
GAGTATGTGGAAACAACGGAGGAGCTCTGACTTCCCAACTGTCCCATTCTATGGGCGAAGGA
ACTGCTCCTGACTTCAGTGGTTAAGGGCAGAATTGAAAATAATTCTGGAGGAAGATAAGAAT
GATTCCTGCGCGACTGCACCGGGACTACAAAGGGCTTGTCCTGCTGGGAATCCTCCTGGGGA
CTCTGTGGGAGACCGGATGCACCCAGATACGCTATTCAGTTCCGGAAGAGCTGGAGAAAGGC
TCTAGGGTGGGCGACATCTCCAGGGACCTGGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGG
AGTCCGCATCATCCCCAGAGGTAGGACGCAGCTTTTCGCCCTGAATCCGCGCAGCGGCAGCT
TGGTCACGGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTGTCAATTA
AATCTAGACATTCTGATGGAGGATAAAGTGAAAATATATGGAGTAGAAGTAGAAGTAAGGGA
CATTAACGACAATGCGCCTTACTTTCGTGAAAGTGAATTAGAAATAAAAATTAGTGAAAATG
CAGCCACTGAGATGCGGTTCCCTCTACCCCACGCCTGGGATCCGGATATCGGGAAGAACTCT
CTGCAGAGCTACGAGCTCAGCCCGAACACTCACTTCTCCCTCATCGTGCAAAATGGAGCCGA
CGGTAGTAAGTACCCCGAATTGGTGCTGAAACGCGCCCTGGACCGCGAAGAAAAGGCTGCTC
ACCACCTGGTCCTTACGGCCTCCGACGGGGGCGACCCGGTGCGCACAGGCACCGCGCGCATC
CGCGTGATGGTTCTGGATGCGAACGACAACGCACCAGCGTTTGCTCAGCCCGAGTACCGCGC
GAGCGTTCCGGAGAATCTGGCCTTGGGCACGCAGCTGCTTGTAGTCAACGCTACCGACCCTG
ACGAAGGAGTCAATGCGGAAGTGAGGTATTCCTTCCGGTATGTGGACGACAAGGCGGCCCAA
GTTTTCAAACTAGATTGTAATTCAGGGACAATATCAACAATAGGGGAGTTGGACCACGAGGA
GTCAGGATTCTACCAGATGGAAGTGCAAGCAATGGATAATGCAGGATATTCTGCGCGAGCCA
AAGTCCTGATCACTGTTCTGGACGTGAACGACAATGCCCCAGAAGTGGTCCTCACCTCTCTC
GCCAGCTCGGTTCCCGAAAACTCTCCCAGAGGGACATTAATTGCCCTTTTAAATGTAAATGA
CCAAGATTCTGAGGAAAACGGACAGGTGATCTGTTTCATCCAAGGAAATCTGCCCTTTAAAT
TAGAAAAATCTTACGGAAATTACTATAGTTTAGTCACAGACATAGTCTTGGATAGGGAACAG
GTTCCTAGCTACAACATCACAGTGACCGCCACTGACCGGGGAACCCCGCCCCTATCCACGGA
AACTCATATCTCGCTGAACGTGGCAGACACCAACGACAACCCGCCGGTCTTCCCTCAGGCCT
CCTATTCCGCTTATATCCCAGAGAACAATCCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCC
CACGACCCCGACTGTGAAGAGAACGCCCAGATCACTTATTCCCTGGCTGAGAACACCATCCA
AGGGGCAAGCCTATCGTCCTACGTGTCCATCAACTCCGACACTGGGGTACTGTATGCGCTGA
GCTCCTTCGACTACGAGCAGTTCCGAGACTTGCAAGTGAAAGTGATGGCGCGGGACAACGGG
CACCCGCCCCTCAGCAGCAACGTGTCGTTGAGCCTGTTCGTGCTGGACCAGAACGACAATGC
GCCCGAGATCCTGTACCCCGCCCTCCCCACGGACGGTTCCACTGGCGTGGAGCTGGCTCCCC
GCTCCGCAGAGCCCGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCCGGCCAG
AACGCCTGGCTGTCCTACCGTCTGCTCAAGGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCT
GCACACGGGCGAGGTGCGCACGGCGCGAGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCC
TCGTAGTGGCCGTCCAGGACCACGGCCAGCCCCCTCTCTCCGCCACTGTCACGCTCACCGTG
GCCGTGGCCGACAGCATCCCCCAAGTCCTGGCGGACCTCGGCAGCCTCGAGTCTCCAGCTAA
CTCTGAAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGGTGGCCGCGGTCTCCTGCGTCT
TCCTGGCCTTCGTCATCTTGCTGCTGGCGCTCAGGCTGCGGCGCTGGCACAAGTCACGCCTG
CTGCAGGCTTCAGGAGGCGGCTTGACAGGAGCGCCGGCGTCGCACTTTGTGGGCGTGGACGG
GGTGCAGGCTTTCCTGCAGACCTATTCCCACGAGGTTTCCCTCACCACGGACTCGCGGAAGA
GTCACCTGATCTTCCCCCAGCCCAACTATGCAGACATGCTCGTCAGCCAGGAGAGCTTTGAA
AAAAGCGAGCCCCTTTTGCTGTCAGGTGATTCGGTATTTCTAAAGACAGTCATGGGTTAAT
TGAGGTGAGTTTATATCAAATCTTCTTTCTTTTTTTTTTTAATTGCTCTGTCTCCCAAGCTG
GAGTGCAGCGGTACGATCATAGCTCACTGCGGCCTCAAACTCCTAGGCTCAAGCAATTATCC
CACCTTTGCCTCCGGTGTAACAGGGACTACAGGTGCAAGCCACCTACTGTCTGCCTATCTAT
CTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTACTTTCTTGTACAGACG
GGAGTCTCACGCCTGTAATCCCAGTACTTTGGGAGGCCGAGGCGGGTGGATCACCTGAGGTT
GGGAGTTTGAGACCAGCCTGACCAACATGGAGAAACCCCGTCTATACTAAAAAAATACAAAA
TTAGCCGGGCGTGGTGGTGCATGTCTGTAATCCCAGCTACTTGGGAGGCTGAGTCAGGAGAA
TTGCTTTAACCTGGGAGGTGGAGGTTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCCT
GGGCAACAAGAGTGAAACTCTATCTCA

FIGURE 157

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306
><subunit 1 of 1, 916 aa, 1 stop
><MW: 100204, pI: 4.92, NX(S/T): 4
MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVPEELEKGSRVGDISRDLGLEPRELAER
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVR
DINDNAPYFRESELEIKISENAATEMRFPLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA
DGSKYPELVLKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFAQPEYR
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSFRYVDDKAAQVFKLDCNSGTISTIGELDHE
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLNVN
DQDSEENGQVICFIQGNLPFKLEKSYGNYYSLVTDIVLDREQVPSYNITVTATDRGTPPLST
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVSLVSVTAHDPDCEENAQITYSLAENTI
QGASLSSYVSINSDTGVLYALSSFDYEQFRDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDN
APEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVDRDSGQNAWLSYRLLKASEPGLFSVG
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADSIPQVLADLGSLESPA
NSETSDLTLYLVVAVAAVSCVFLAFVILLLALRLRRWHKSRLLQASGGGLTGAPASHFVGVD
GVQAFLQTYSHEVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGL
IEVSLYQIFFLFFFNCSVSQAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRDYRCKPPTVCLS
IYLSIYLSIYLSIYLLLSCTDGSLTPVIPVLWEAEAGGSPEVGSLRPA

FIGURE 158

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA
TCAGTAGGTGACCCCGCCCCTGGATTCTGGAAGACCTCACC<u>ATG</u>GGACGCCCCCGACCTCGT
GCGGCCAAGACGTGGATGTTCCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGC
ACAGGAGGACAAGGTGCTGGGGGGTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAGGTGGCAACTGGGTCCTT
ACAGCTGCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACA
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG
CACCGTCTCAGGCTGGGGCACTGTCACCAGTCCCCGAGAGAATTTTCCTGACACTCTCAACT
GTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG
CCCCCTGGTGTGTGATGGTGCACTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC
ATAGGCAGCAAGGGC<u>TGA</u>TTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCT
CTGGTTC

FIGURE 159

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336
<subunit 1 of 1, 260 aa, 1 stop
<MW: 28048, pI: 7.87, NX(S/T): 1
MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL
VGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSIPHPCYNSSDVEDHNHDLMLL
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCED
AYPGQITDGMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRY
LDWIKKIIGSKG

Important Features:

Signal peptide:
amino acids 1-23

Transmembrane domain:
amino acids 51-71

N-glycosylation site.
amino acids 110-113

Serine proteases, trypsin family, histidine active site.
amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.
amino acids 182-188

Kringle domain proteins motif
amino acids 205-217

FIGURE 160

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGCCCGC
CGCGCCGCCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCGGGCCCGCGCCCGC
GCCCGCGCCCAGGTGAGCGCTCCGCCCGCCGCGAGGCCCCGCCCCGGCCCGCCCCCGCCCCG
CCCCGGCCGGCGGGGGAACCGGGCGGATTCCTCGCGCGTCAAACCACCTGATCCCATAAAAC
ATTCATCCTCCCGGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCGCCGCCGCCCTCG
CCCTGTGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCCAGCCAGAGCCGGGCGGAGC
GGAGCGCGCCGAGCCTCGTCCCGCGGCCGGGCCGGGGCCGGGCCGTAGCGGCGGCGCCTGGA
TGCGGACCCGGCCGCGGGGAGACGGGCGCCCGCCCCGAAACGACTTTCAGTCCCCGACGCGC
CCCGCCCAACCCCTACG<u>ATG</u>AAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG
CTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCATGCCCAGGTGCCTGCGTATGCTACAATGA
GCCCAAGGTGACGACAAGCTGCCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTG
CTGCCAGCCAGCGCATCTTCCTGCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC
CGTGCCTGCCGCAACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATGC
GGCTGCCTTCACTGGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC
GGTCTGTGGACCCTGCCACATTCCACGGCCTGGGCCGCCTACACACGCTGCACCTGGACCGC
TGCGGCCTGCAGGAGCTGGGCCCGGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTA
CCTGCAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCA
CACACCTCTTCCTGCACGGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTG
CACAGCCTCGACCGTCTCCTACTGCACCAGAACCGCGTGGCCCATGTGCACCCGCATGCCTT
CCGTGACCTTGGCCGCCTCATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCA
CTGAGGCCCTGGCCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG
TGTGACTGCCGGGCACGCCCACTCTGGGCCTGGCTGCAGAAGTTCCGCGGCTCCTCCTCCGA
GGTGCCCTGCAGCCTCCCGCAACGCCTGGCTGGCCGTGACCTCAAACGCCTAGCTGCCAATG
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACC
GATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGT
ACTGGAGCCTGGAAGACCAGCTTCGGCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTG
ACAGCCCGCCGGGCAACGGCTCTGGCCCACGGCACATCAATGACTCACCCTTTGGGACTCTG
CCTGGCTCTGCTGAGCCCCCGCTCACTGCAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTT
CCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTCACGCAAGAACCGCACCCGCAGCCACT
GCCGTCTGGGCCAGGCAGGCAGCGGGGGTGGCGGGACTGGTGACTCAGAAGGCTCAGGTGCC
CTACCCAGCCTCACCTGCAGCCTCACCCCCCTGGGCCTGGCGCTGGTGCTGTGGACAGTGCT
TGGGCCCTGC<u>**TGA**</u>CCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATAC
GGGGTCTCTCTCCACGCCGCCAAGCCAGCCGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAG
GTCCTCCCTGATGGACGCCTGCCGCCCGCCACCCCCATCTCCACCCCATCATGTTTACAGGG
TTCGGCGGCAGCGTTTGTTCCAGAACGCCGCCTCCCACCCAGATCGCGGTATATAGAGATAT
GCATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAATAAAGAGCTCTTTTCTTAAA
AAAA

FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184
><subunit 1 of 1, 473 aa, 1 stop
><MW: 50708, pI: 9.28, NX(S/T): 6

MKRASAGGSRLLAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI
FLHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAAFTGLALLEQLDLSDNAQLRSVDPA
TFHGLGRLHTLHLDRCGLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH
GNRISSVPERAFRGLHSLDRLLLHQNRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAP
LRALQYLRLNDNPWVCDCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCA
VATGPYHPIWTGRATDEEPLGLPKCCQPDAADKASVLEPGRPASAGNALKGRVPPGDSPPGN
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA
GSGGGGTGDSEGSGALPSLTCSLTPLGLALVLWTVLGPC

Important features:

Signal peptide:

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

FIGURE 162

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCCTCTGGAGAGGACTAC
TCACTGGCATATTTCTGAGGTATCTGTAGAATAACCACAGCCTCAGATACTGGGGACTTTAC
AGTCCCACAGAACCGTCCTCCCAGGAAGCTGAATCCAGCAAGAACAATGGAGGCCAGCGGGA
AGCTCATTTGCAGACAAAGGCAAGTCCTTTTTTCCTTTCTCCTTTTGGGCTTATCTCTGGCG
GGCGCGGCGGAACCTAGAAGCTATTCTGTGGTGGAGGAAACTGAGGGCAGCTCCTTTGTCAC
CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGGTTAGGGTTG
TTTCCAGAGGGAACAAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTTGTTGCTAAAT
GAGAAATTGGACCGTGAGGATCTGTGCGGTCACACAGAGCCCTGTGTGCTACGTTTCCAAGT
GTTGCTAGAGAGTCCCTTCGAGTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC
ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCCTCCTGGG
ACTACGTTTCCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA
TATAATCAGCCCCAACTCCTATTTTCGGGTCCTCACCCGCAAACGCAGTGATGGCAGGAAAT
ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAACA
CTCACAGCACTGGATGGTGGCTCTCCGCCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT
CCTGGATGTCAACGATAATGCCCCTGAATTTGAGCAGCCTTTCTATAGAGTGCAGATCTCTG
AGGACAGTCCGGTAGGCTTCCTGGTTGTGAAGGTCTCTGCCACGGATGTAGACACAGGAGTC
AACGGAGAGATTTCCTATTCACTTTTCCAAGCTTCAGAAGAGATTGGCAAAACCTTTAAGAT
CAATCCCTTGACAGGAGAAATTGAACTAAAAAAACAACTCGATTTCGAAAAACTTCAGTCCT
ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTTCTGGAAAATGCACCGTTCTGATT
CAAGTGATAGATGTGAACGACCATGCCCCAGAAGTTACCATGTCTGCATTTACCAGCCCAAT
ACCTGAGAACGCGCCTGAAACTGTGGTTGCACTTTTCAGTGTTTCAGATCTTGATTCAGGAG
AAAATGGGAAAATTAGTTGCTCCATTCAGGAGGATCTACCCTTCCTCCTGAAATCCGCGGAA
AACTTTTACACCCTACTAACGGAGAGACCACTAGACAGAGAAAGCAGAGCGGAATACAACAT
CACTATCACTGTCACTGACTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC
TGATCGCCGATGTCAATGACAACGCTCCCGCCTTCACCCAAACCTCCTACACCCTGTTCGTC
CGCGAGAACAACAGCCCCGCCCTGCACATCCGCAGCGTCAGCGCTACAGACAGAGACTCAGG
CACCAACGCCCAGGTCACCTACTCGCTGCTGCCGCCCCAGGACCCGCACCTGCCCCTCACAT
CCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTCGCCCTCAGGTCTCTGGACTACGAG
GCCCTGCAGGGGTTCCAGTTCCGCGTGGGCGCTTCAGACCACGGCTCCCCGGCGCTGAGCAG
CGAGGCGCTGGTGCGCGTGGTGGTGCTGGACGCCAACGACAACTCGCCCTTCGTGCTGTACC
CGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCCGAGCCGGGCTAC
CTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTCGTACCA
GCTGCTCAAGGCCACGGAGCTCGGTCTGTTCGGCGTGTGGGCGCACAATGGCGAGGTGCGCA
CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCCAAGCACAGGCTGGTGGTGCTGGTCAAGGAC
AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCCTGGTGGACGGCTTCTC
CCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCCGACCCAGGCCCAGGCCGACTTGCTCACCG
TCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCCTCTTTTCGGTGCTCCTGTTC
GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCCTCGGTGGGTCGCTGCTTGGTGCCCGA
GGGCCCCCTTCCAGGGCATCTTGTGGACATGAGCGGCACCAGGACCCTATCCCAGAGCTACC
AGTATGAGGTGTGTCTGGCAGGAGGCTCAGGGACCAATGAGTTCAAGTTCCTGAAGCCGATT
ATCCCCAACTTCCCTCCCCAGTGCCCTGGGAAAGAAATACAAGGAAATTCTACCTTCCCCAA
TAACTTTGGGTTCAATATTCAGTGACCATAGTTGACTTTTACATTCCATAGGTATTTTATTT
TGTGGCATTTCCATGCCAATGTTTATTTCCCCCAATTTGTGTGTATGTAATATTGTACGGAT
TTACTCTTGATTTTTCTCATGTTCTTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT
CCTGGTTCTT

FIGURE 163

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314
<subunit 1 of 1, 798 aa, 1 stop
<MW: 87552, pI: 4.84, NX(S/T): 5

MEASGKLICRQRQVLFSFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR
RGVRVVSRGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRFQVLLESPFEFFQAELQV
IDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNAPEFEQPFY
RVQISEDSPVGFLVVKVSATDVDTGVNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPENAPETVVALFSVS
DLDSGENGKISCSIQEDLPFLLKSAENFYTLLTERPLDRESRAEYNITITVTDLGTPMLITQ
LNMTVLIADVNDNAPAFTQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLLPPQDP
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELGLFGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAQ
ADLLTVYLVVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMSGTRT
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNFPPQCPGKEIQGNSTFPNNFGFNIQ

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 685-712

Cadherins extracellular repeated domain signature.

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

ATP/GTP-binding site motif A (P-loop).

amino acids 285-292

N-glycosylation site.

amino acids 418-421, 436-439, 567-570 and 786-789

FIGURE 164

ACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCGCGTAGCCGTGC
GCCGATTGCCTCTCGGCCTGGGCAATGGTCCCGGCTGCCGGTCGACGACCGCCCCGCGTCAT
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTGG
AGGTTGCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCCTCTCCAGGTG
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG
TGATTCCTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT
GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTCTGGATGGCGCTGG
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG
GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTCACAGGACCT
TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCCTGTTTTACACCCCGTGGT
GCCGCTTTTCTGCCAGTTTGGCCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT
CACTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC
TGTTCCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATACAGATC
GAACACTGGAAACACTGAAAATCTTCATTTTTAATCAGACAGGTATAGAAGCCAAGAAGAAT
GTGGTGGTAACTCAAGCCGACCAAATAGGCCCTCTTCCCAGCACTTTGATAAAAAGTGTGGA
CTGGTTGCTTGTATTTTCCTTATTCTTTTTAATTAGTTTTATTATGTATGCTACCATTCGAA
CTGAGAGTATTCGGTGGCTAATTCCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT
GAAAGAAGTTGGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA
CATTTTCTCCAGTGACGTGTTGACTTGAAACTTCAGGCAGATTAAAAGAATCATTTGTTGAA
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC
AAAAATATTCAATAG

FIGURE 165

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333
><subunit 1 of 1, 360 aa, 1 stop
><MW: 39885, pI: 4.79, NX(S/T): 7

MVPAAGRRPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE
ELLHDPMGQDRAAEEANAVLGLDTQGDHMVMLSVIPGEAEDKVSSEPSGVTCGAGGAEDSRC
NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE
NFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS
QHSSLSTRFGTVAVPNILLFQGAKPMARFNHTDRTLETLKIFIFNQTGIEAKKNVVVTQADQ
IGPLPSTLIKSVDWLLVFSLFFLISFIMYATIRTESIRWLIPGQEQEHVE

Important features:

Signal peptide:
amino acids 1-25

Transmembrane domain:
amino acids 321-340

Homologous region to dilsufide isomerase
amino acids 212-302

N-glycosylation site.
amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281 and 293-296

Thioredoxin domain
amino acids 211-227

FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCCACGATGCTGCAGGGCCCTGGCT
CGCTGCTGCTGCTCTTCCTCGCCTCGCACTGCTGCCTGGGCTCGGCGCGCGGGCTCTTCCTC
TTTGGCCAGCCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCAACCTGCTGGGCCACGAGACCA
TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG
GACACCAAGAAGTTCCTGTGCTCGCTCTTCGCCCCCGTCTGCCTCGATGACCTAGACGAGAC
CATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGCCCCGGTCATGTCCG
CCTTCGGCTTCCCCTGGCCCGACATGCTTGAGTGCGACCGTTTCCCCCAGGACAACGACCTT
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG
ATTTTGCACTGAAAATAAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAAATCATC
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA
ATCGGTGCTGTGGCTCAAAGACAGCTTGCAGTGCACCTGTGAGGAGATGAACGACATCAACG
CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTA
GTCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTTCTGCTCC
GGGATCTCAGCTCCCGTTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTCCTGAGTTATAAGGCCACAGGAGTG
GATAGCTGTTTTCACCTAAAGGAAAAGCCCACCCGAATCTTGTAGAAATATTCAAACTAATA
AAATCATGAATATTTTAA

FIGURE 167

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920
><subunit 1 of 1, 295 aa, 1 stop
><MW: 33518, pI: 7.74, NX(S/T): 0
MLQGPGSLLLLFLASHCCLGSARGLFLFGQPDFSYKRSNCKPIPVNLQLCHGIEYQNMRLPN
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDETIQPCHSLCVQVKDR
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDDDNDIM
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLNGVSERDLKKSVLWLKDSLQCTCE
EMNDINAPYLVMGQKQGGELVITSVKRWQKGQREFKRISRSIRKLQC

Important features:
Signal peptide:
amino acids 1-20

Cysteine rich domain, homolgous to frizzled N terminus
amino acids 6-153

FIGURE 168

GTGGAGGCCGCCGACGATGGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCCTGCTCGCGATC
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT
TGCTGAGGACTTGGTCCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTCGGGCTCCGTGCGGCG
ACCATCCTGGGTGCGTGGCTGAACTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT
TGTTGGGACCCAAAACCCATTTGCCTTCCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCCCAGAGCACCAGCGA
GCCACGGCCAACATGCTCGCCACCATGTCGAACCCTCTGGGCGTCCTTGTGGCCAATGTGCT
GTCCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATACCATCC
CTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCCACCCCG
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCCTGGATGGGCTCAAGCTGCAGCT
CATGTGGAACAAGGCCTATGTCATCCTGGCTGTGTGCTTGGGGGGAATGATCGGGATCTCTG
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCCTA
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG
CCTGCGTGCCCTTTGCCCTGGTGTCCCAGCTGCAGGGACAGACCCTTGCCCTGGCTGCCACC
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTCGA
GTGTTCCTTCCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCCTTG
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCGG
CCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC
AGGCCGAGTCTGGGGAGCCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCCTGGGGCCCAGCACGGCGACTCCGGA
GTGCACGGCGAGGGGGGCCTCGCTAGAGGACCCCAGAGGGCCCGGGAGCCCCCACCCAGCCT
GCCACCGAGCGACTCCCCGTGCGCAAGGCCCAGCAGCCACCGACGCGCCCTCCCGCCCCGGC
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAGTCCAGGTTGCCCGCCACATCGA
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

FIGURE 169

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988
><subunit 1 of 1, 560 aa, 1 stop
><MW: 58427, pI: 6.86, NX(S/T): 2

MAGPTEAETGLAEPRALCAQRGHRTYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMLATMSNPLGVLVANVLSPVLV
KKGEDIPLMLGVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA
YVILAVCLGGMIGISASFSALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK
HFTEATKIGLCLFSLACVPFALVSQLQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV
GEGAATGMIFVLGQAEGILIMLAMTALTVRRSEPSLSTCQQGEDPLDWTVSLLLMAGLCTFF
SCILAVFFHTPYRRLQAESGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG
ASLEDPRGPGSPHPACHRATPRAQGPAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

Important features:

Potential Transmembrane domains:

amino acids 30-50, 61-79, 98-112, 126-146, 169-182, 201-215, 248-268, 280-300, 318-337, 341-357, 375-387, 420-441

N-glycosylation site.

amino acids 40-43 and 43-46

Glycosaminoglycan attachment site.

amino acids 468-471

FIGURE 170A

GTCCCACATCCTGCTCAACTGGGTCAGGTCCCTCTTAGACCAGCTCTTGTCCATCATTTGCT
GAAGTGGACCAACTAGTTCCCCAGTAGGGGGTCTCCCCTGGCAATTCTTGATCGGCGTTTGG
ACATCTCAGATCGCTTCCAATGAAGATGGCCTTGCCTTGGGGTCCTGCTTGTTTCATAATCA
TCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGAAGGAGCACGGGGCTGATCAAGC
CATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAAGAACTCTAGTGGTTTCTGAATCTA
GCCCACTTGGCGGTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGG
TGGCTACTTATTTCTTTTAGGGGATTGTCAGGAGGTGACCACTCTCACGGTGAAATACCAAG
TGTCAGAGGAAGTGCCATCTGGTACAGTGATCGGGAAGCTGTCCCAGGAACTGGGCCGGGAG
GAGAGGCGGAGGCAAGCTGGGGCCGCCTTCCAGGTGTTGCAGCTGCCTCAGGCGCTCCCCAT
TCAGGTGGACTCTGAGGAAGGCTTGCTCAGCACAGGCAGGCGGCTGGATCGAGAGCAGCTGT
GCCGACAGTGGGATCCCTGCCTGGTTTCCTTTGATGTGCTTGCCACAGGGGATTTGGCTCTG
ATCCATGTGGAGATCCAAGTGCTGGACATCAATGACCACCAGCCACGGTTTCCCAAAGGCGA
GCAGGAGCTGGAAATCTCTGAGAGCGCCTCTCTGCGAACCCGGATCCCCCTGGACAGAGCTC
TTGACCCAGACACAGGCCCTAACACCCTGCACACCTACACTCTGTCTCCCAGTGAGCACTTT
GCCTTGGATGTCATTGTGGGCCCTGATGAGACCAAACATGCAGAACTCATAGTGGTGAAGGA
GCTGGACAGGGAAATCCATTCATTTTTGATCTGGTGTTAACTGCCTATGACAATGGGAACC
CCCCCAAGTCAGGTACCAGCTTGGTCAAGGTCAACGTCTTGGACTCCAATGACAATAGCCCT
GCGTTTGCTGAGAGTTCACTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCT
CATAAAACTGACCGCCACAGACCCTGACCAAGGCCCCAATGGGGAGGTGGAGTTCTTCCTCA
GTAAGCACATGCCTCCAGAGGTGCTGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTC
ATTCTGCGTCGACCTCTAGACTATGAAAAGAACCCTGCCTACGAGGTGGATGTTCAGGCAAG
GGACCTGGGTCCCAATCCTATCCAGCCCATTGCAAAGTTCTCATCAAGGTTCTGGATGTCA
ATGACAACATCCCAAGCATCCACGTCACATGGGCCTCCCAGCCATCACTGGTGTCAGAAGCT
CTTCCCAAGGACAGTTTTATTGCTCTTGTCATGGCAGATGACTTGGATTCAGGACACAATGG
TTTGGTCCACTGCTGGCTGAGCCAAGAGCTGGGCCACTTCAGGCTGAAAAGAACTAATGGCA
ACACATACATGTTGCTAACCAATGCCACACTGGACAGAGAGCAGTGGCCCAAATATACCCTC
ACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATCAGCCAAGAAACAGCTCAGCATTCA
GATCAGTGACATCAACGACAATGCACCTGTGTTTGAGAAAAGCAGGTATGAAGTCTCCACGC
GGGAAAACAACTTACCCTCTCTTCACCTCATTACCATCAAGGCTCATGATGCAGACTTGGGC
ATTAATGGAAAAGTCTCATACCGCATCCAGGACTCCCCAGTTGCTCACTTAGTAGCTATTGA
CTCCAACACAGGAGAGGTCACTGCTCAGAGGTCACTGAACTATGAAGAGATGGCCGGCTTTG
AGTTCCAGGTGATCGCAGAGGACAGCGGGCAACCCATGCTTGCATCCAGTGTCTCTGTGTGG
GTCAGCCTCTTGGATGCCAATGATAATGCCCCAGAGGTGGTCCAGCCTGTGCTCAGCGATGG
AAAAGCCAGCCTCTCCGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGCCCATCGAGA
CTCCCAATGGCTTGGGCCCAGCGGGCACTGACACACCTCCACTGGCCACTCACAGCTCCCGG
CCATTCCTTTTGACAACCATTGTGGCAAGAGATGCAGACTCGGGGGCAAATGGAGAGCCCCT
CTACAGCATCCGCAATGGAAATGAAGCCCACCTCTTCATCCTCAACCCTCATACGGGGCAGC
TGTTCGTCAATGTCACCAATGCCAGCAGCCTCATTGGGAGTGAGTGGGAGCTGGAGATAGTA
GTAGAGGACCAGGGAAGCCCCCCCTTACAGACCCGAGCCCTGTTGAGGGTCATGTTTGTCAC
CAGTGTGGACCACCTGAGGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTCGATGCTGA
CGGTGATCTGCCTGGCTGTACTGTTGGGCATCTTCGGGTTGATCCTGGCTTTGTTCATGTCC
ATCTGCCGGACAGAAAAGAAGGACAACAGGGCCTACAACTGTCGGGAGGCCGAGTCCACCTA
CCGCCAGCAGCCCAAGAGGCCCCAGAAACACATTCAGAAGGCAGACATCCACCTCGTGCCTG
TGCTCAGGGGTCAGGCAGGTGAGCCTTGTGAAGTCGGGCAGTCCCACAAAGATGTGGACAAG
GAGGCGATGATGGAAGCAGGCTGGGACCCCTGCCTGCAGGCCCCCTTCCACCTCACCCCGAC
CCTGTACAGGACGCTGCGTAATCAAGGCAACCAGGGAGCACCGGCGGAGAGCCGAGAGGTGC
TGCAAGACACGGTCAACCTCCTTTTCAACCATCCCAGGCAGAGGAATGCCTCCCGGGAGAAC
CTGAACCTTCCCGAGCCCCAGCCTGCCACAGGCCAGCCACGTTCCAGGCCTCTGAAGGTTGC
AGGCAGCCCCACAGGGAGGCTGGCTGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCAC
CAGCCTCCTCTGCAACCCTGAGACGGCAGCGACATCTCAATGGCAAAGTGTCCCCTGAGAAA
GAATCAGGGCCCCGTCAGATCCTGCGGAGCCTGGTCCGGCTGTCTGTGGCTGCCTTCGCCGA
GCGGAACCCCGTGGAGGAGCTCACTGTGGATTCTCCTCCTGTTCAGCAAATCTCCCAGCTGC
TGTCCTTGCTGCATCAGGGCCAATTCCAGCCCAAACCAAACCACCGAGGAAATAAGTACTTG
GCCAAGCCAGGAGGCAGCAGGAGTGCAATCCCAGACACAGATGGCCCAAGTGCAAGGGCTGG

FIGURE 170B

AGGCCAGACAGACCCAGAACAGGAGGAAGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGA
AGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCCCAGCACAGGTCTGGCCCTGGAC
CGGCTGAGCGCCCCTGACCCGGCCTGGATGGCGAGACTCTCTTTGCCCCTCACCACCAACTA
CCGTGACAATGTGATCTCCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGT
TCGGCAAGGCAGAGGCACCAGAGCTGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGTC
TCGGAGATGAGCTCACTGCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCGTGGAGGC
CGCCTCCGAGGCGCTGCGGCGGCTCTCGGTCTGCGGGAGGACCCTCAGTTTAGACTTGGCCA
CCAGTGCAGCCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGGAAAGACGGGGACTGAGGGC
AAGAGCAGAGGCAGCAGCAGCAGCAGCAGGTGCCTG<u>TGA</u>ACATACCTCAGACGCCTCTGGAT
CCAAGAACCAGGGGCCTGAGGATCTGTGGACAAGAGCTGGTTTCTAAAATCTTGTAACTCAC
TAGCTAGCGGCGGCCTGAGAACTTTAGGGTGACTGATGCTACCCCCACAGAGGAGGCAAGAG
CCCCAGGACTAACAGCTGACTGACCAAAGCAGCCCCTTGTAAGCAGCTCTGAGTCTTTTGGA
GGACAGGGACGGTTTGTGGCTGAGATAAGTGTTTCCTGGCAAAACATATGTGGAGCACAAAG
GGTCAGTCCTCTGGCAGAACAGATGCCACGGAGTATCACAGGCAGGAAAGGGTGGCCTTCTT
GGGTAGCAGGAGTCAGGGGGCTGTACCCTGGGGGTGCCAGGAAATGCTCTCTGACCTATCAA
TAAAGGAAAAGCAGTAAAAAAAAAAAAAAAAAAAA

FIGURE 171

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331

<subunit 1 of 1, 1184 aa, 1 stop

<MW: 129022, pI: 5.20, NX(S/T): 5

MMQLLQLLLGLLGPGGYLFLLGDCQEVTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQA
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFDVLATGDLALIHVEIQ
VLDINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNTLHTYTLSPSEHFALDVIV
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSNDNSPAFAESS
LALEIQEDAAPGTLLIKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPL
DYEKNPAYEVDVQARDLGPNPIPAHCKVLIKVLDVNDNIPSIHVTWASQPSLVSEALPKDSF
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQD
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHDADLGINGKVS
YRIQDSPVAHLVAIDSNTGEVTAQRSLNYEEMAGFEFQVIAEDSGQPMLASSVSVWVSLLDA
NDNAPEVVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPPLATHSSRPFLLTT
IVARDADSGANGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK
KDNRAYNCREAESTYRQQPKRPQKHIQKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEA
GWDPCLQAPFHLTPTLYRTLRNQGNQGAPAESREVLQDTVNLLFNHPRQRNASRENLNLPEP
QPATGQPRSRPLKVAGSPTGRLAGDQGSEEAPQRPPASSATLRRQRHLNGKVSPEKESGPRQ
ILRSLVRLSVAAFAERNPVEELTVDSPPVQQISQLLSLLHQGQFQPKPNHRGNKYLAKPGGS
RSAIPDTDGPSARAGGQTDPEQEEGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPD
PAWMARLSLPLTTNYRDNVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSL
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSLDLATSAASGMKVQGDPGGKTGTEGKSRGSS
SSSRCL

Important features:

Signal peptide:

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 amd 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGAGAGCCGCAGTCCCGGCTGCAGCACCTGGGAGAAGG
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT
CCCAGATACTATTTTTGGATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT
GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGCACCAT
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT
GGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTCATGGTGCCTTTTTACATTGGC
TATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTTCCTGTCTCTT
ATGGCTGACCTTTATGTATTTCTTCTGGAAACTAGGAGATCCCTTTCCCATTCTCAGCCCAA
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTGGTGTGATTGGAGTGACTCTC
ATGGCTCTTCTTTCTGGATTTGGTGCTGTCAACTGCCCATACACTTACATGTCTTACTTCCT
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGG
AAGTGAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC
TTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC
AAGGGGAAATATTTTAATTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAATTTT
CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCACAAGAGGCA
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATT
TCCTTCATTCTTGTTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCATTGTCCTGCTATTAGCAC
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA
TACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTT
TGATGTGATCTTCCTGGTCAGCGCTCTCTCTAGCATACTCTTCCTCTATTTGGCTCACAAAC
AGGCACCAGAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGT
GGTTTCAAAATTTAGATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAAC
AAACAAAATGCTATGGTAGCATTTTTCACCTTCATAGCATACTCCTTCCCCGTCAGGTGATA
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAGAAACTAA
AGGTGAAAAATACACTGGAACTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT
AGGATTTCCGTTTTAAGGTTCACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT
AAAATCAGAGACTGTAACAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCG
ACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

FIGURE 173

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI
LGVLNSSSRYFHWKMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFF
WKLGDPFPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ
QEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF
DRVGKTDPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISS
SKSSNVIVLLLAQIMGMYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA
LSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398, 425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 174

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA
TCATGATTACCTCCCNGANACTATTTTTTGGATTTGGGTGGCTTTTCTTCNGCGCCAATGTT
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTT
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

FIGURE 175

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC
TTTNTTGAATTCCGGGTTNNGNATACCTTCCCAGAAAATATTTTTTGGATTTGGGGTAGNTT
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT
NTCCGTGACGTTTGCATTTTCTTGCACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC
CTGGTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA
TAAACAACGACTGCTTTTTTTCCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN
TAGGAGATCCCTTTCCCATTCTC

FIGURE 176A

CTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCCGCGACCCTTGGGGGCCTCCGGGA
TTTGCTACCTTTTTGGCTCCCTGCTCGTCGAACTGCTCTTCTCACGGGCTGTCGCCTTCAAT
CTGGACGTGATGGGTGCCTTGCGCAAGGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGT
GGCCCTGCACCGGCAGTTGCAGCCCCGACCCCAGAGCTGGCTGCTGGTGGGTGCTCCCCAGG
CCCTGGCTCTTCCTGGGCAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTGCCCGTTGAGC
CTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAG
CAAGGAGAACCAGTGGTTGGGAGTCAGTGTTCGGAGCCAGGGGCCTGGGGGCAAGATTGTTA
CCTGTGCACACCGATATGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATG
ATTGGTCGCTGCTTTGTGCTCAGCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGGA
ATGGAAGTTCTGTGAGGGACGCCCCCAAGGCCATGAACAATTTGGGTTCTGCCAGCAGGGCA
CAGCTGCCGCCTTCTCCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAACCTATAAT
TGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGGA
CGACGGTCCCTACGAGGCGGGGGGAGAGAAGGAGCAGGACCCCCGCCTCATCCCGGTCCCTG
CCAACAGCTACTTTGGCTTCTCTATTGACTCGGGGAAAGGTCTGGTGCGTGCAGAAGAGCTG
AGCTTTGTGGCTGGAGCCCCCCGCGCCAACCACAAGGGTGCTGTGGTCATCCTGCGCAAGGA
CAGCGCCAGTCGCCTGGTGCCCGAGGTTATGCTGTCTGGGGAGCGCCTGACCTCCGGCTTTG
GCTACTCACTGGCTGTGGCTGACCTCAACAGTGATGGCTGGCCAGACCTGATAGTGGGTGCC
CCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGCTGTGTATGTGTACTTGAACCAGGG
GGGTCACTGGGCTGGGATCTCCCCTCTCCGGCTCTGCGGCTCCCCTGACTCCATGTTCGGGA
TCAGCCTGGCTGTCCTGGGGGACCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGGTGCC
CCCTTTGATGGTGATGGGAAAGTCTTCATCTACCATGGGAGCAGCCTGGGGGTTGTCGCCAA
ACCTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGGCTACTCCCTGTCAG
GCAGCTTGGATATGGATGGGAACCAATACCCTGACCTGCTGGTGGGCTCCCTGGCTGACACC
GCAGTGCTCTTCAGGGCCAGACCCATCCTCCATGTCTCCCATGAGGTCTCTATTGCTCCACG
AAGCATCGACCTGGAGCAGCCCAACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGG
TCTGTTTCAGCTACATTGCAGTCCCCAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTG
TTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGTTCCCCGTGTGACGTTCCTGAGCCG
TAACCTGGAAGAACCCAAGCACCAGGCCTCGGGCACCGTGTGGCTGAAGCACCAGCATGACC
GAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTCGGGCCATT
GTAGTGACCTTGTCCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCCTGGCCAGGG
GCTGCCTCCAGTGGCCCCCATCCTCAATGCCCACCAGCCCAGCACCCAGCGGGCAGAGATCC
ACTTCCTGAAGCAAGGCTGTGGTGAAGACAAGATCTGCCAGAGCAATCTGCAGCTGGTCCAC
GCCCGCTTCTGTACCCGGGTCAGCGACACGGAATTCCAACCTCTGCCCATGGATGTGGATGG
AACAACAGCCCTGTTTGCACTGAGTGGGCAGCCAGTCATTGGCCTGGAGCTGATGGTCACCA
ACCTGCCATCGGACCCAGCCCAGCCCCAGGCTGATGGGGATGATGCCCATGAAGCCCAGCTC
CTGGTCATGCTTCCTGACTCACTGCACTACTCAGGGGTCCGGGCCCTGGACCCTGCGGAGAA
GCCACTCTGCCTGTCCAATGAGAATGCCTCCCATGTTGAGTGTGAGCTGGGGAACCCCATGA
AGAGAGGTGCCCAGGTCACCTTCTACCTCATCCTTAGCACCTCCGGGATCAGCATTGAGACC
ACGGAACTGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAGCAGGAGCTGCATCCAGTCTC
TGCACGAGCCCGTGTCTTCATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTCCCCAGC
AACTCTTCTTCTCTGGTGTGGTGAGGGGCGAGAGAGCCATGCAGTCTGAGCGGGATGTGGGC
AGCAAGGTCAAGTATGAGGTCACGGTTTCCAACCAAGGCCAGTCGCTCAGAACCCTGGGCTC
TGCCTTCCTCAACATCATGTGGCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAA
TGCAGGTTGAGCTGGAGGGCGGGCAGGGGCCTGGGCAGAAAGGGCTTTGCTCTCCCAGGCCC
AACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGGCGGCGGGAGCTGGAGCCACCTGA
GCAGCAGGAGCCTGGTGAGCGGCAGGAGCCCAGCATGTCCTGGTGGCCAGTGTCCTCTGCTG
AGAAGAAGAAAAACATCACCCTGGACTGCGCCCGGGGCACGGCCAACTGTGTGGTGTTCAGC
TGCCCACTCTACAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGAACAG
CACCTTTCTGGAGGAGTACTCAGCTGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCA
CAGTGAAGTCCTCCATAAAGAACTTGATGCTCCGAGATGCCTCCACAGTGATCCCAGTGATG
GTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGTGGGTCATCCTCCTGGC
TGTACTGGCTGGGCTGCTGGTGCTAGCACTGCTGGTGCTGCTCCTGTGGAAGATGGGATTCT
TCAAACGGGCGAAGCACCCCGAGGCCACCGTGCCCCAGTACCATGCGGTGAAGATTCCTCGG
GAAGACCGACAGCAGTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAACTGGGGCAG

FIGURE 176B

CCCCCGGCGGGAGGGCCCGGATGCACACCCCATCCTGGCTGCTGACGGGCATCCCGAGCTGG
GCCCCGATGGGCATCCAGGGCCAGGCACCGCC<u>TAG</u>GTTCCCATGTCCCAGCCTGGCCTGTGG
CTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGTGGGCTGCTG
GTGTCGCATCAAGATTTGGCAGGATCGGCTTCCTCAGGGGCACAGACCTCTCCCACCCACAA
GAACTCCTCCCACCCAACTTCCCCTTAGAGTGCTGTGAGATGAGAGTGGGTAAATCAGGGAC
AGGGCCATGGGGTAGGGTGAGAAGGGCAGGGGTGTCCTGATGCAAAGGTGGGGAGAAGGGAT
CCTAATCCCTTCCTCTCCCATTCACCCTGTGTAACAGGACCCCAAGGACCTGCCTCCCCGGA
AGTGCCTTAACCTAGAGGGTCGGGGAGGAGGTTGTGTCACTGACTCAGGCTGCTCCTTCTCT
AGTTTCCCCTCTCATCTGACCTTAGTTTGCTGCCATCAGTCTAGTGGTTTCGTGGTTTCGTC
TATTTATTAAAAAATATTTGAGAACAAAAAAAAAAAAAAAAAAA

FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL
QPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMQKESKENQWL
GVSVRSQGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDGGEWKFCEG
RPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGTARVELCAQGSADLAHLDDGPYEA
GGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELSFVAGAPRANHKGAVVILRKDSASRLV
PEVMLSGERLTSGFGYSLAVADLNSDGWPDLIVGAPYFFERQEELGGAVYVYLNQGGHWAGI
SPLRLCGSPDSMFGISLAVLGDLNQDGFPDIAVGAPFDGDGKVFIYHGSSLGVVAKPSQVLE
GEAVGIKSFGYSLSGSLDMDGNQYPDLLVGSLADTAVLFRARPILHVSHEVSIAPRSIDLEQ
PNCAGGHSVCVDLRVCFSYIAVPSSYSPTVALDYVLDADTDRRLRGQVPRVTFLSRNLEEPK
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSYSLQTPRLRRQAPGQGLPPVAP
ILNAHQPSTQRAEIHFLKQGCGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA
LSGQPVIGLELMVTNLPSDPAQPQADGDDAHEAQLLVMLPDSLHYSGVRALDPAEKPLCLSN
ENASHVECELGNPMKRGAQVTFYLILSTSGISIETTELEVELLLATISEQELHPVSARARVF
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKYEVTVSNQGQSLRTLGSAFLNIM
WPHEIANGKWLLYPMQVELEGGQGPGQKGLCSPRPNILHLDVDSRDRRRRELEPPEQQEPGE
RQEPSMSWWPVSSAEKKKNITLDCARGTANCVVFSCPLYSFDRAAVLHVWGRLWNSTFLEEY
SAVKSLEVIVRANITVKSSIKNLMLRDASTVIPVMVYLDPMAVVAEGVPWWVILLAVLAGLL
VLALLVLLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGTILRNNWGSPRREGP
DAHPILAADGHPELGPDGHPGPGTA

Important features:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 1039-1064

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCGTGCAGCAGCTCCAGA
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT
CACAACAAG<u>ATG</u>CTCAAGGTGTCAGCCGTACTGTGTGTGTGCAGCCGCTTGGTGCAGTCA
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGGCGGTCGGACGGCGGTAATTTTC
TGGATGATAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC
AAATTCCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCCTTCGA
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC
CCATGTCCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT
GGAGTTCAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAA
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTCGATACCAGCATC
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAACAGACTTGATACAAACTATGACCT
GCTATTGGACCAGTCAGAGCTCAGAAGCATTTACCTTGATAAGAATGAACAGTGTACCAAGG
CATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC
CAACACAATGTCATGGCAGTGTTGGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTC
ATGGGATCCAGAATAAATGGTGTTGCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGATGAC
CATGATGTATACATT<u>TGA</u>TTGATGACAGTTGAAATCAATAAATTCTACATTTCTAATATTTA
CAAAAATGATAGCCTATTTAAAATTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCA
CATATATTTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAACTTTATGTTTAAAT
AAGAATCATTTGCTTTGAGTTTTTATATTCCTTACACAAAAAGAAAATACATATGCAGTCTA
GTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTCACGAGAACAAACTTTGT
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAAG
ATAATTCTAAGTGAAATTTAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG
GATAACAGAGAGATACCACATGACTCCAAAAAAAAAAAAAAA

FIGURE 179

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829
><subunit 1 of 1, 436 aa, 1 stop
><MW: 49429, pI: 4.80, NX(S/T): 0

MLKVSAVLCVCAAAWCSQSLAAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR
DEVEDDYFRTWSPGKPFDQALDPAKDPCLKMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCPCP
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTKTLLRPERSRFDTSILPI
CKDSLGWMFNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ
RQQDPPCQTELSNIQKRQGVKKLLGQYIPLCDEDGYYKPTQCHGSVGQCWCVDRYGNEVMGS
RINGVADCAIDFEISGDFASGDFHEWTDDEDDEDDIMNDEDEIEDDDEDEGDDDDGGDDHDVYI

Important features:

Signal peptide:

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

FIGURE 180A

CAGACTCCAGATTTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAA
CAGTACCTGACGCCTCTTTCAGCCCGGGATCGCCCCAGCAGGGATGGGCGACAAGATCTGGC
TGCCCTTCCCCGTGCTCCTTCTGGCCGCTCTGCCTCCGGTGCTGCTGCCTGGGGCGGCCGGC
TTCACACCTTCCCTCGATAGCGACTTCACCTTTACCCTTCCCGCCGGCCAGAAGGAGTGCTT
CTACCAGCCCATGCCCCTGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTTAGATGGAGCAG
GATTAGATATTGATTTCCATCTTGCCTCTCCAGAAGGCAAAACCTTAGTTTTTGAACAAAGA
AAATCAGATGGAGTTCACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAA
TACATTCAGCACCATTTCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAG
AACAGGCACAAGAACAAGAAGATTGGAAGAAATATATTACTGGCACAGATATATTGGATATG
AAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCCAGACTAAGCAAAAGTGGGCA
CATACAAATTCTGCTTAGAGCATTTGAAGCTCGTGATCGAAACATACAAGAAAGCAACTTTG
ATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTCATGGTGGTGGTGTCAGCCATTCAA
GTTTATATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAACTTAAAACTCCAAACT
AGAGTACGTAACATTGAAAAATGAGGCATAAAAATGCAATAAACTGTTACAGTCAAGACCAT
TAATGGTCTTCTCCAAAATATTTTGAGATATAAAAGTAGGAAACAGGTATAATTTTAATGTG
AAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAGTTGTACTTAAGTGTGTA
ACAGGAATATTTTGCAGAATATAGGTTTAACTGAATGAAGCCATATTAATAACTGCATTTTC
CTAACTTTGAAAAATTTTGCAAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCTAAT
TGCAACACCAGTCTGTTTTTAACAGGTTCTATTACCCAGAACTTTTTTGTAAATGCGGCAGT
TACAAATTAACTGTGGAAGTTTTCAGTTTTAAGTTATAAATCACCTGAGAATTACCTAATGA
TGGATTGAATAAATCTTTAGACTACAAAAGCCCAACTTTTCTCTATTTACATATGCATCTCT
CCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTGAGATTTTTATAACC
AAATACATTTCAGTGTAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTCC
CAAAAGCTGACATTTTCACGATTCTTAAAAACACAAAGTTACACTTACTAAAATTAGGACAT
GTTTTCTCTTTGAAATGAAGAATATAGTTTAAAAGCTTCCTCCTCCATAGGGACACATTTTC
TCTAACCCTTAACTAAAGTGTAGGATTTTAAAATTAAATGTGAGGTAAAATAAGTTTATTTT
TAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAATAATCATGTTATGTTAATTTTAAC
ATGATTGCTGACTTGGATAATTCATTATTACCAGCAGTTATGAAGGAAATATTGCTAAAATG
ATCTGGGCCTACCATAAATAAATATCTCCTTTTCTGAGCTCTAAGAATTATCAGAAAACAGG
AAAGAATTTAGAAAAACTTGAGAAAACCTAATCCAAAATAAAATTCACTTAAGTAGAACTAT
AAATAAATATCTAGAATCTGACTGGCTCATCATGACATCCTACTCATAACATAAATCAAAGG
AGATGATTAATTTCCAGTTAGCTGGAAGAAACTTTGGCTGTAGGTTTTTATTTTCTACAAGA
ATTCTGGTTTGAATTATTTTTGTAAGCAGGTACATTTTATAAAATGTAAGCCCTACTGTAAG
GTTTAGCACTGGGTGTACATATTTATTAAAAATTTTTATTATAACAACTTTTATTAAAATGG
CCTTTCTGAACACTTTATTTATTGATGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTT
TTAAACACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTTGA
AGTCTATGGGGGTCTTACTCAAGTACTAGTAATTTAACTTCATCATGAATGAACTATAATTT
TTAAGTTATGCCCATTTATAACGTTGTTTATGACTACATTGTGAGTTAGAAACAAACTTAAA
ATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATTCTTGATGAGCAATAATGA
TAACCAGAGAGTGATTTCATTTACACTCATAGTAGTATAAAAAGAGATACATTTCCCTCTTA
GGCCCCTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAAA
TGCCGTATATGATCAATTACCTTAATTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCC
TCTGCAACACTTGCAGAACAAAGGTCAATAAGATCCTTGCCTATGAATACCCCTCCCTTTTG
CGCTGTTAAATTTGCAATGAGAAGCAAATTTACAGTACCATAACTAATAAAGCAGGGTACAG
ATATAAACTACTGCATCTTTTCTATAAAACTGTGATTAAGAATTCTACCTCTCCTGTATGGC
TGTTACTGTACTGTACTCTCTGACTCCTTACCTAACAATGAATTTGTTACATAATCTTCTAC
ATGTATGATTTGTGCCACTGATCTTAAACCTATGATTCAGTAACTTCTTACCATATAAAAAC
GATAATTGCTTTATTTGGAAAAGAATTTAGGAATACTAAGGACAATTATTTTTATAGACAAA
GTAAAAAGACAGATATTTAAGAGGCATAACCAAAAAAGCAAAACTTGTAAACAGAGTAAAAA
TCTTTAATATTTCTAAAGACATACTGTTTATCTGCTTCATATGCTTTTTTTAATTTCACTAT
TCCATTTCTAAATTAAAGTTATGCTAAATTGAGTAAGCTGTTTATCACTTAACAGCTCATTT
TGTCTTTTTCAATATACAAATTTTAAAAATACTACAATATTTAACTAAGGCCCAACCGATTT
CCATAATGTAGCAGTTACCGTGTTCACCTCACACTAAGGCCTAGAGTTTGCTCTGATATGCA
TTTGGATGATTAATGTTATGCTGTTCTTTCATGTGAATGTCAAGACATGGAGGGTGTTTGTA

FIGURE 180B

ATTTTATGGTAAAATTAATCCTTCTTACACATAATGGTGTCTTAAAATTGACAAAAAATGAG
CACTTACAATTGTATGTCTCCTCAAATGAAGATTCTTTATGTGAAATTTTAAAAGACATTGA
TTCCGCATGTAAGGATTTTTCATCTGAAGTACAATAATGCACAATCAGTGTTGCTCAAACTG
CTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATA
ATAAAAATTATCAAAGGAAAA

FIGURE 181

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196

><subunit 1 of 1, 229 aa, 1 stop

><MW: 26017, pI: 4.73, NX(S/T): 0

MGDKIWLPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFTLPAGQKECFYQPMPLKASLEIEY
QVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCFDNTFSTISEKVIFFEL
ILDNMGEQAQEQEDWKKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN
IQESNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

FIGURE 182

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT
CTCACCAGAGAGTCGCAGACACT<u>ATG</u>CTGCCTCCCATGGCCCTGCCCAGTGTGTCCTGGATG
CTGCTTTCCTGCCTCATTCTCCTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCC
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT
TTTTGTCACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCCTCCCTGGTGAGGAGCATTAG
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCCACACAGGGCTCTGAGCCTGATG
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC
TCCACCATCTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGAC<u>TAG</u>GGCAGGT
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC
TCACCCTGGAAGAGAATATTCTCCCCAAACTGCCCTACCTGACTACCTTGTCATGATCCTCC
TTCTTTTTCCTTTTTCTTCACCTTCATTTCAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC
TCAGAGAATAATAATAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 183

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965
<subunit 1 of 1, 175 aa, 1 stop
<MW: 19330, pI: 7.25, NX(S/T): 1
MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM
DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:
Signal peptide:
amino acids 1-26

C-type lectin domain signature.
amino acids 146-171

FIGURE 184

CCAGTCTGTCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC
ACAGAGGAGTGGGCCGGGACC<u>ATG</u>CGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGCTGGC
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCGTGTCCTGCTGCAATACTG
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC
CTCCCACTCTTGAGCCTCCGACTG<u>TAG</u>AGTCCCCGCCCACCCCCATGGCCCTATGCGGCCCA
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAA

FIGURE 185

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405
<subunit 1 of 1, 125 aa, 1 stop
<MW: 13115, pI: 5.90, NX(S/T): 1
MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP
FQGDSTVTKSCASKCKPSDVDGIGQTLPVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

Important features:
Signal peptide:
amino acids 1-17

N-glycosylation site.
amino acids 46-49

FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC
ACGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTCGCGATGG
TAGCGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACTCGGTTCTC
AATTCCAACGCTATCAAGAACCTGCCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA
GACACTTCTGGTCCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCAT
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTCAGA
GACACTAAACCAGCTATCCAAATGCAGTGAACTCCTTTTATATAATAGATGCTATGAAAACC
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACTCCCCTG
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA
AACTTTTAATTATTTTTCTAAAGGTGCTGCACTGCCTATTTTTCCTCTTGTTATGTAAATTT
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT
TCAGCTTATAGTTCTTAAAAGCATAACCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA
AGGATCTCTTGGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA
AATAAAATTTAACATTTAAAAAAAAAAAAA

FIGURE 187

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530
<subunit 1 of 1, 266 aa, 1 stop
<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA
APGILYPGGNKYQTIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRKRCMRH
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQ
KDHHQASNSSRLHTCQRH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

FIGURE 188

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTTCTTTCTCCTTCNG
GAGTCCTTNTGAGANGATGGTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG
GTAGCGGCGGTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTC
AATTCCAACGNTATCAAGAACCTGCCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCANGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTNTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGG

FIGURE 189A

GAGGAACCTACCGGTACCGGCCGCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATC
CCGTGCGCCGCGGCTGGGCCGTCGGAGAGTGCGTGTGCTTCTCTCCTGCACGCGGTGCTTGG
GCTCGGCCAGGCGGGGTCCGCCGCCAGGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGAC
CCCGCGATGGCAAGGTATATTTTTGTGGAATGAAAAGGAAGTATTAGAAATGAGCTGAAGAC
CATTCACAGATTAATATTTTTGGGGACAGATTTGTGATGCTTGATTCACCCTTGAAGTAATG
TAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTT
CACTTAAATCAGAACTTGCATAAGAAAGAGA<u>ATG</u>GGAGTCTGGTTAAATAAAGATGACTATA
TCAGAGACTTGAAAAGGATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGC
ACAGATCAGGATTTTTACAGTTTACTTGGAGTGTCCAAAACTGCAAGCAGTAGAGAAATAAG
ACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAAAAACCCGAATAACCCAAATG
CACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGATCTACGG
AAAAAGTATGACAAATATGGAGAAAAGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAG
CTGGAACTATTATCGTTATGATTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGG
AAAGAAGAGAATTTGATGCTGCTGTTAATTCTGGAGAACTGTGGTTTGTAAATTTTTACTCC
CCAGGCTGTTCACACTGCCATGATTTAGCTCCCACATGGAGAGACTTTGCTAAAGAAGTGGA
TGGGTTACTTCGAATTGGAGCTGTTAACTGTGGTGATGATAGAATGCTTTGCCGAATGAAAG
GAGTCAACAGCTATCCCAGTCTCTTCATTTTTCGGTCTGGAATGGCCCCAGTGAAATATCAT
GGAGACAGATCAAAGGAGAGTTTAGTGAGTTTTGCAATGCAGCATGTTAGAAGTACAGTGAC
AGAACTTTGGACAGGAAATTTTGTCAACTCCATACAAACTGCTTTTGCTGCTGGTATTGGCT
GGCTGATCACTTTTTGTTCAAAAGGAGGAGATTGTTTGACTTCACAGACACGACTCAGGCTT
AGTGGCATGTTGTTTCTCAACTCATTGGATGCTAAAGAAATATATTTGGAAGTAATACATAA
TCTTCCAGATTTTGAACTACTTTCGGCAAACACACTAGAGGATCGTTTGGCTCATCATCGGT
GGCTGTTATTTTTTCATTTTGGAAAAAATGAAAATTCAAATGATCCTGAGCTGAAAAAACTA
AAAACTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGACTGTTCCTCTGCACCAGA
CATCTGTAGTAATCTGTATGTTTTTCAGCCGTCTCTAGCAGTATTTAAAGGACAAGGAACCA
AAGAATATGAAATTCATCATGGAAAGAAGATTCTATATGATATACTTGCCTTTGCCAAAGAA
AGTGTGAATTCTCATGTTACCACGCTTGGACCTCAAAATTTTCCTGCCAATGACAAAGAACC
ATGGCTTGTTGATTTCTTTGCCCCCTGGTGTCCACCATGTCGAGCTTTACTACCAGAGTTAC
GAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTCAT
GAGGGACTCTGTAACATGTATAACATTCAGGCTTATCCAACAACAGTGGTATTCAACCAGTC
CAACATTCATGAGTATGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTCATAGAGGATC
TTATGAATCCTTCAGTGGTCTCCCTTACACCCACCACCTTCAACGAACTAGTTACACAAAGA
AAACACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTGGTGTCATCCTTGCCAAGTCTT
AATGCCAGAATGGAAAAGAATGGCCCGGACATTAACTGGACTGATCAACGTGGGCAGTATAG
ATTGCCAACAGTATCATTCTTTTTGTGCCCAGGAAAACGTTCAAAGATACCCTGAGATAAGA
TTTTTTCCCCCAAAATCAAATAAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGA
TGCTTATTCCCTGAGAATCTGGGGTCTAGGATTTTTACCTCAAGTATCCACAGATCTAACAC
CTCAGACTTTCAGTGAAAAAGTTCTACAAGGGAAAAATCATTGGGTGATTGATTTCTATGCT
CCTTGGTGTGGACCTTGCCAGAATTTTGCTCCAGAATTTGAGCTCTTGGCTAGGATGATTAA
AGGAAAAGTGAAAGCTGGAAAAGTAGACTGTCAGGCTTATGCTCAGACATGCCAGAAAGCTG
GGATCAGGGCCTATCCAACTGTTAAGTTTTATTTCTACGAAAGAGCAAAGAGAAATTTTCAA
GAAGAGCAGATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAAAAATTGGA
AACTCTCCGAAATCAAGGCAAGAGGAATAAGGATGAACTT<u>TGA</u>TAATGTTGAAGATGAAGAA
AAAGTTTAAAAGAAATTCTGACAGATGACATCAGAAGACACCTATTTAGAATGTTACATTTA
TGATGGGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCAGAATTATCTACAGCA
CTGGTGTAAAAGAAGGGTCTGCAAACTTTTTCTGTAAAGGGCCGGTTTATAAATATTTTAGA
CTTTGCAGGCTATAATATATGGTTCACACATGAGAACAAGAATAGAGTCATCATGTATTCTT
TGTTATTTGCTTTTAACAACCTTTAAAAAATATTAAAACGATTCTTAGCTCAGAGCCATACA
AAAGTAGGCTGGATTCAGTCCATGGACCATAGATTGCTGTCCCCCTCGACGGACTTATAATG
TTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCTATCTACATAAATGTCTAAGTTGTAT
AAAGTCCACTTTCCCTTCACGTTTTTGGCTGACCTGAAAAGAGGTAACTTAGTTTTTGGTC
ACTTGTTCTCCTAAAAATGCTATCCCTAACCATATATTTATATTTCGTTTTAAAAACACCCA
TGATGTGGCACAGTAAACAAACCCTGTTATGCTGTATTATTATGAGGAGATTCTTCATTGTT
TTCTTTCCTTCTCAAAGGTTGAAAAAATGCTTTTAATTTTTCACAGCCGAGAAACAGTGCAG

FIGURE 189B

CAGTATATGTGCACACAGTAAGTACACAAATTTGAGCAACAGTAAGTGCACAAATTCTGTAG
TTTGCTGTATCATCCAGGAAAACCTGAGGGAAAAAAATTATAGCAATTAACTGGGCATTGTA
GAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATATGTGTTCAT
GTATTTTCTGAAATTGCTTTCATAGAAATTTTCCCACTGATAGTTGATTTTTGAGGCATCTA
ATATTTACATATTTGCCTTCTGAACTTTGTTTTGACCTGTATCCTTTATTTACATTGGGTTT
TTCTTTCATAGTTTTGGTTTTTCACTCCTGTCCAGTCTATTTATTATTCAAATAGGAAAAAT
TACTTTACAGGTTGTTTTACTGTAGCTTATAATGATACTGTAGTTATTCCAGTTACTAGTTT
ACTGTCAGAGGGCTGCCTTTTTCAGATAAATATTGACATAATAACTGAAGTTATTTTTATAA
GAAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTGTTTAGACTCAAA
GAATCACAAATTTGTCAGTAACATGTAGTTGTTTAGTTATAATTCAGAGTGTACAGAATGGT
AAAAATTCCAATCAGTCAAAAGAGGTCAATGAATTAAAAGGCTTGCAACTTTTTCAAAAAAA
AAAAAAAAAA

FIGURE 190

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKL
HPDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKGLEDNQGGQYESWNYYRYDFGI
YDDDPEIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC
GDDRMLCRMKGVNSYPSLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNS
IQTAFAAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN
TLEDRLAHHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQP
SLAVFKGQGTKEYEIHHGKKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWC
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIHEYEGHHS
AEQILEFIEDLMNPSVVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG
FLPQVSTDLTPQTFSEKVLQGKNHWVIDFYAPWCGPCQNFAPEFELLARMIKGKVKAGKVDC
QAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAIAALISEKLETLRNQGKRNKDEL

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGA
GTCGTTGGTGAAGTTTTTCATTCCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAAACTGCAGCTGAGTGCCGAAA
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA
CATCCTAGGACATTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCCTTACCTCATCCCATAT
TGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCTT
GGGAAAAACTGGTATCAAAACCTCATGTCTCTGCCCAGTTTTTGTGAATACTGGGTTCACCA
AAAATCCAAGCACAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA
GATGGAATACTTACCAATAAGAAAATGATTTTTGTTCCATCGTATATCAATATCTTTCTGAG
ACTACAGAAGTTTCTTCCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAATAAATAAGCTCCAGCCAGAGATG
TATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTCACATTTTT
TCAGTCCTGATAATATTAAAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA
ATTACCTGTCTTCCTGTTTCTCAAGAATATTTACGTAGTTTTTCATAGGTCTGTTTTTCCTT
TCATGCCTCTTAAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT
TTTATTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT
TATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT
ATCTCAACCTGGACATATTTTAAGATTCAGCATTTGAAAGATTTCCCTAGCCTCTTCCTTTT
TCATTAGCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT
AACTCTGAAGTCCACCAAAAGTGGACCCTCTATATTTCCTCCCTTTTTATAGTCTTATAAGA
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAGTTCTAGCCCCATGA
TAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAAT
TTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAA
CAATGGACCCAAGAGAAGAA

FIGURE 192

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409
<subunit 1 of 1, 300 aa, 1 stop
<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI
LVLWDINKRGVEETAAECRKLGVTAHAYVVDCSNREEIYRSLNQVKKEVGDVTIVVNNAGTV
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFVNTGFTKNPSTRLWPVLETDEVVRSLID
GILTNKKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

FIGURE 193

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCCAGCAGG
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCCAGCCCGCCCGGGGC
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTCATGATCCT
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACACGTCCTTCT
CTAGGCCGCACACGGGGCCGCCGCTGCCCACGCCCGGGCCGGACAGGGACAGGGAGCTCACG
GCCGACTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA
CCTTCCCAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG
GCTACGACTGGTCCCCGCGCGACGCCCGGCGCAGCCCAGACCAGGGCCGGCAGCAGGCGGAG
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCG
CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGG
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA
CGTGCACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCCTCTTCGTGCGCGACCCC
TTCGTGCGCCTGATCTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG
CAAGTTCGCCGTGCCCATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCCTCGGCGC
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGAC
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCCGAGCTACCGGAACAGG
ACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC
GAGACTGAAAGCTTTCGCGTTGCTTTTTCTCGCGTGCCTGGAACCTGACGCACGCGCACTCC
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC
ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAATATATTTCAGGTATTTAATACGA

FIGURE 194

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112
<subunit 1 of 1, 414 aa, 1 stop
<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGSVFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRELTA
DSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAER
RSVLRGFCANSSLAFPTKERAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLS
GSLLHRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF
VRLISAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDP
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLDEDAAQLLQLLQVDRQLRFPPSYRNRT
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

Important features:

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

FIGURE 195

TCGGGCCAGAATTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA
AAGAGGCCCAGAGTAGAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT
ATGCCGGGAAGGTGGTGGTCGTGACCGGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC
GCCTTCGTGAACAGCGGGGCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGGC
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG
TGAAGACCCTGGTTTCTGAGACCATCCGCCGATTTGGCCGCCTGGATTGTGTTGTCAACAAC
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCCTACCTGCGGA
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCCAG
CCACTGGGCCGCATGGGCCAGCCCGCTGAGGTCGGGGCTGCGGCAGTGTTCCTGGCCTCCGA
AGCCAACTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGCAGAGCTGGGGTACGGGT
GCAAGGCCAGTCGGAGCACCCCCGTGGACGCCCCCGATATCCCTTCCTGATTTCTCTCATTT
CTACTTGGGGCCCCCTTCCTAGGACTCTCCCACCCCAAACTCCAACCTGTATCAGATGCAGC
CCCCAAGCCCTTAGACTCTAAGCCCAGTTAGCAAGGTGCCGGGTCACCCTGCAGGTTCCCAT
AAAAACGATTTGCAGCC

FIGURE 196

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045
<subunit 1 of 1, 270 aa, 1 stop
<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVTGGGRGIGAGIVRAFVNSGARVVICDKDESGGRALEQELPGAVFILCD
VTQEDDVKTLVSETIRRFGRLDCVVNNAGHHPPPQRPEETSAQGFRQLLELNLLGTYTLTKL
ALPYLRKSQGNVINISSLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTGG
AELGYGCKASRSTPVDAPDIPS

Important features:

N-glycosylation site.

amino acids 138-141

Short-chain alcohol dehydrogenase family protein

amino acids 10-22, 81-91, 134-171 and 176-185

FIGURE 197

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACCTG
CTGTTTCTTCTTACCATTTCCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAA
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCTGGCCCCTGGCCCTCACCAGGTGCCACTGGACC
TGGTGTCACGGATGAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG
GTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCT
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCC
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACC
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCAGGTTCCTGTGCGCCGCCG
CCTCTGCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG
CTGTGGGCTGCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCGAGA
CCATCCTCCTTGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA
GCAAG

FIGURE 198

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEY
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPSRIPVDLPEARCLCL
GCVNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

FIGURE 199

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGG
CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCG
GCGCCCAAC<u>ATG</u>GCGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCCTGGAT
CGCGGCTGTGGCGGCGACGGCAGGCCCCGAGGAGGCCGCGCTGCCGCCGGAGCAGAGCCGGG
TCCAGCCCATGACCGCCTCCAACTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT
TACGCCCCATGGTGTCCATCCTGCCAGCAGACTGATTCAGAATGGGAGGCTTTTGCAAAGAA
TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTG
GCCGCTTCTTTGTCACCACTCTCCCAGCATTTTTTCATGCAAAGGATGGGATATTCCGCCGT
TATCGTGGCCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC
AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACTATTTCACAGTGACTCTTGGAATT
CCTGCTTGGTGTTCTTATGTGTTTTTCGTCATAGCCACCTTGGTTTTTGGCCTTTTTATGGG
TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG
GAGGAAAAAGATGATTCAAATGAAGAAGAAAACAAAGACAGCCTTGTAGATGATGAAGAAGA
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACTTGGCTG
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTG
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCCAGC
TGACACAGAGGTGGTGGAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGAC
TG<u>TAG</u>ATTTAATGATGCGTTTTCAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGG
CCTGCAGTTTGTACCAAATCCTTAATTTTTCCTGAATGAGCAAGCTTCTCTTAAAAGATGCT
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT
GACAATCAGGATATAGAAAAACAAACGTAGTGTTGGGATCTGTTTGGAGACTGGGATGGGAA
CAAGTTCATTTACTTAGGGGTCAGAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCCTAATC
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCT
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGCATCCTTTTCTTGTGTAAAGTATTTAT
TTTTGTCAAATTGCAGGAAACATCAGGCACCACAGTGCATGAAAAATCTTTCACAGCTAGAA
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTG
TGCTATGTTTTATTTCTTACCTTTAATTTTTCCAGCATTTCCACCATGGGCATTCAGGCTCT
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC
TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAAGGAAGTAAGGATT
TTACAAGACAGATTAAAAAAAAATTGTTTTGTCCAAAATATAGTTGTTGTTGATTTTTTTTT
AAGTTTCTAAGCAATATTTTTCAAGCCAGAAGTCCTCTAAGTCTTGCCAGTACAAGGTAGT
CTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTCATCTCAAGGGGTTCCCTGGGTCTTGAAC
TACTTTAATAATAACTAAAAAACCACTTCTGATTTTCCTTCAGTGATGTGCTTTTGGTGAAA
GAATTAATGAACTCCAGTACCTGAAAGTGAAAGATTTGATTTTGTTTCCATCTTCTGTAATC
TTCCAAAGAATTATATCTTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG
GCTAATTTCTTT

FIGURE 200

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433

<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP
WCPSCQQTDSEWEAFAKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIFRRYRG
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW
CSYVFFVIATLVFGLFMGLVLVVISECFYVPLPRHLSERSEQNRRSEEAHRAEQLQDAEEEK
DDSNEEENKDSLVDDEEEKEDLGDEDEAEEEEEEDNLAAGVDEERSEANDQGPPGEDGVTRE
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSQHADKGL

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

FIGURE 201

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCCACATGATT
TGACTCAGAGATTCTCTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC
CAAATGCTATATCTATTCAGGGGCTCTCAAGAACAATGGAATATCATCCTGATTTAGAAAAT
TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTTCTTTCC
AGCCCTTGTCCTCCTAATTGGATTATATATGAGAAGAGCTGTTATCTATTCAGCATGTCACT
AAATTCCTGGGATGGAAGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG
ACAGCTCAAATGAATTGGGATTTATAGTAAAACAAGTGTCTTCCCAACCTGATAATTCATTT
TGGATAGGCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT
CTCTTCTAACTTATTTCAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCAAATTGTG
TATGGATTCACGTGTCAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT
GAGAAGAAGTTTTCAATGTAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA
AGGAGGACAGAAAACAGAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATG
TTTAGAGAGCTTGGCCAACTGTAATCTTAACCAAGAAATTGAAGGGAGAGGCTGTGATTTCT
GTATTTGTCGACCTACAGGTAGGCTAGTATTATTTTTCTAGTTAGTAGATCCCTAGACATGG
AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTATTTATTTTTTTGAGATAGGGTCT
CACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC
CTCAGCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTGGTG
TTTTTGTAGAGACTGGGTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG
TGATCTGCCCGCCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC
CCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTTACCTTGGGTAAGCCATAAGCGA
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT
GTGTTGCCACGATTTGACCCTCAACTTCTAGCAGTATATCAGTTATGAACTGAGGGTGAAAT
ATATTTCTGAATAGCTAAATGAAGAAATGGAAAAAATCTTCACCACAGTCAGAGCAATTTT
ATTATTTTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAACTCCTA
CTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT
TTTTTTTTTTTTTTTTTTGAGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTGCAACGG
CACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCT
CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTTAGT
AGAGACAGGGTTTCTCCATGTCGGTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGC
CTGCCTCGGCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAATCT
TGTATAATATGTAATTGTAGGGAAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTAAATACA
AAAATACATAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA
ACAAGTATTAACATTTTGGAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTT
ACCATTTTTTTCAGTAATTACTGTAAAATGGTATTATTGGAATGAAACTATATTTCCTCATG
TGCTGATTTGTCTTATTTTTTTCATACTTTCCCACTGGTGCTATTTTTATTTCCAATGGATA
TTTCTGTATTACTAGGGAGGCATTTACAGTCCTCTAATGTTGATTAATATGTGAAAAGAAAT
TGTACCAATTTTACTAAATTATGCAGTTTAAAATGGATGATTTTATGTTATGTGGATTTCAT
TTCAATAAAAAAAAACTCTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 202

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912
<subunit 1 of 1, 201 aa, 1 stop
<MW: 22563, pI: 4.87, NX(S/T): 1
MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSCAASPPWRLIAVILGILCLVILVIAV
VLGTMGVLSSPCPPNWIIYEKSCYLFSMSLNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL
CSVPSYSICEKKFSM

Important features:

Type II transmembrane domain:

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

FIGURE 203A

GGAAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGCCCAGACCTGGAGGG
TCTCGCTCTGTCACACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTCCACC
TCCCGGGTTCAAGTGATTCTCATGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGTGGTGAC
TTCCAAGAGTGACTCCGTCGGAGGAAAATGACTCCCCAGTCGCTGCTGCAGACGACACTGTT
CCTGCTGAGTCTGCTCTTCCTGGTCCAAGGTGCCCACGGCAGGGGCCACAGGGAAGACTTTC
GCTTCTGCAGCCAGCGGAACCAGACACACAGGAGCAGCCTCCACTACAAACCCACACCAGAC
CTGCGCATCTCCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCCTTTCCCTGCAGC
CCACCCTGCTTCCCGATCCTTCCCTGACCCCAGGGGCCTCTACCACTTCTGCCTCTACTGGA
ACCGACATGCTGGGAGATTACATCTTCTCTATGGCAAGCGTGACTTCTTGCTGAGTGACAAA
GCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGGAGAGCCTGGCTCAGGGCCCCCCGCTGTT
AGCCACTTCTGTCACCTCCTGGTGGAGCCCTCAGAACATCAGCCTGCCCAGTGCCGCCAGCT
TCACCTTCTCCTTCCACAGTCCTCCCCACACGGCCGCTCACAATGCCTCGGTGGACATGTGC
GAGCTCAAAAGGGACCTCCAGCTGCTCAGCCAGTTCCTGAAGCATCCCCAGAAGGCCTCAAG
GAGGCCCTCGGCTGCCCCCGCCAGCCAGCAGTTGCAGAGCCTGGAGTCGAAACTGACCTCTG
TGAGATTCATGGGGGACATGGTGTCCTTCGAGGAGGACCGGATCAACGCCACGGTGTGGAAG
CTCCAGCCCACAGCCGGCCTCCAGGACCTGCACATCCACTCCCGGCAGGAGGAGGAGCAGAG
CGAGATCATGGAGTACTCGGTGCTGCTGCCTCGAACACTCTTCCAGAGGACGAAAGGCCGGA
GCGGGGAGGCTGAGAAGAGACTCCTCCTGGTGGACTTCAGCAGCCAAGCCCTGTTCCAGGAC
AAGAATTCCAGCCAAGTCCTGGGTGAGAAGGTCTTGGGGATTGTGGTACAGAACACCAAAGT
AGCCAACCTCACGGAGCCCGTGGTGCTCACTTTCCAGCACCAGCTACAGCCGAAGAATGTGA
CTCTGCAATGTGTGTTCTGGGTTGAAGACCCCACATTGAGCAGCCCGGGGCATTGGAGCAGT
GCTGGGTGTGAGACCGTCAGGAGAGAAACCCAAACATCCTGCTTCTGCAACCACTTGACCTA
CTTTGCAGTGCTGATGGTCTCCTCGGTGGAGGTGGACGCCGTGCACAAGCACTACCTGAGCC
TCCTCTCCTACGTGGGCTGTGTCGTCTCTGCCCTGGCCTGCCTTGTCACCATTGCCGCCTAC
CTCTGCTCCAGGGTGCCCCTGCCGTGCAGGAGGAAACCTCGGGACTACACCATCAAGGTGCA
CATGAACCTGCTGCTGGCCGTCTTCCTGCTGGACACGAGCTTCCTGCTCAGCGAGCCGGTGG
CCCTGACAGGCTCTGAGGCTGGCTGCCGAGCCAGTGCCATCTTCCTGCACTTCTCCCTGCTC
ACCTGCCTTTCCTGGATGGGCCTCGAGGGGTACAACCTCTACCGACTCGTGGTGGAGGTCTT
TGGCACCTATGTCCCTGGCTACCTACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCCATCT
TTCTGGTGACGCTGGTGGCCCTGGTGGATGTGGACAACTATGGCCCCATCATCTTGGCTGTG
CATAGGACTCCAGAGGGCGTCATCTACCCTTCCATGTGCTGGATCCGGGACTCCCTGGTCAG
CTACATCACCAACCTGGGCCTCTTCAGCCTGGTGTTTCTGTTCAACATGGCCATGCTAGCCA
CCATGGTGGTGCAGATCCTGCGGCTGCGCCCCCACACCCAAAAGTGGTCACATGTGCTGACA
CTGCTGGGCCTCAGCCTGGTCCTTGGCCTGCCCTGGGCCTTGATCTTCTTCTCCTTTGCTTC
TGGCACCTTCCAGCTTGTCGTCCTCTACCTTTTCAGCATCATCACCTCCTTCCAAGGCTTCC
TCATCTTCATCTGGTACTGGTCCATGCGGCTGCAGGCCCGGGGTGGCCCCTCCCCTCTGAAG
AGCAACTCAGACAGCGCCAGGCTCCCCATCAGCTCGGGCAGCACCTCGTCCAGCCGCATCTA
GGCCTCCAGCCCACCTGCCCATGTGATGAAGCAGAGATGCGGCCTCGTCGCACACTGCCTGT
GGCCCCCGAGCCAGGCCCAGCCCCAGGCCAGTCAGCCGCAGACTTTGGAAAGCCCAACGACC
ATGGAGAGATGGGCCGTTGCCATGGTGGACGGACTCCCGGGCTGGGCTTTTGAATTGGCCTT
GGGGACTACTCGGCTCTCACTCAGCTCCCACGGGACTCAGAAGTGCGCCGCCATGCTGCCTA
GGGTACTGTCCCCACATCTGTCCCAACCCAGCTGGAGGCCTGGTCTCTCCTTACAACCCCTG
GGCCCAGCCCTCATTGCTGGGGGCCAGGCCTTGGATCTTGAGGGTCTGGCACATCCTTAATC
CTGTGCCCCTGCCTGGGACAGAAATGTGGCTCCAGTTGCTCTGTCTCTCGTGGTCACCCTGA
GGGCACTCTGCATCCTCTGTCATTTTAACCTCAGGTGGCACCCAGGGCGAATGGGGCCCAGG
GCAGACCTTCAGGGCCAGAGCCCTGGCGGAGGAGAGGCCCTTTGCCAGGAGCACAGCAGCAG
CTCGCCTACCTCTGAGCCCAGGCCCCCTCCCTCCCTCAGCCCCCCAGTCCTCCCTCCATCTT
CCCTGGGGTTCTCCTCCTCTCCCAGGGCCTCCTTGCTCCTTCGTTCACAGCTGGGGGTCCCC
GATTCCAATGCTGTTTTTGGGGAGTGGTTTCCAGGAGCTGCCTGGTGTCTGCTGTAAATGT
TTGTCTACTGCACAAGCCTCGGCCTGCCCCTGAGCCAGGCTCGGTACCGATGCGTGGGCTGG
GCTAGGTCCCTCTGTCCATCTGGGCCTTTGTATGAGCTGCATTGCCCTTGCTCACCCTGACC
AAGCACACGCCTCAGAGGGGCCCTCAGCCTCTCCTGAAGCCCTCTTGTGGCAAGAACTGTGG
ACCATGCCAGTCCCGTCTGGTTTCCATCCCACCACTCCAAGGACTGAGACTGACCTCCTCTG
GTGACACTGGCCTAGAGCCTGACACTCTCCTAAGAGGTTCTCTCCAAGCCCCCAAATAGCTC

FIGURE 203B

CAGGCGCCCTCGGCCGCCCATCATGGTTAATTCTGTCCAACAAACACACACGGGTAGATTGC
TGGCCTGTTGTAGGTGGTAGGGACACAGATGACCGACCTGGTCACTCCTCCTGCCAACATTC
AGTCTGGTATGTGAGGCGTGCGTGAAGCAAGAACTCCTGGAGCTACAGGGACAGGGAGCCAT
CATTCCTGCCTGGGAATCCTGGAAGACTTCCTGCAGGAGTCAGCGTTCAATCTTGACCTTGA
AGATGGGAAGGATGTTCTTTTTACGTACCAATTCTTTTGTCTTTTGATATTAAAAAGAAGTA
CATGTTCATTGTAGAGAATTTGGAAACTGTAGAAGAGAATCAAGAAGAAAAATAAAAATCAG
CTGTTGTAATCGCCTAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921
<subunit 1 of 1, 693 aa, 1 stop
<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSLLQTTLFLLSLLFLVQGAHGRGHREDFRFCSQRNQTHRSSLHYKPTPDLRISIENSE
EALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH
QEESLAQGPPLLATSVTSWWSPQNISLPSAASFTFSFHSPPHTAAHNASVDMCELKRDLQLL
SQFLKHPQKASRRPSAAPASQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD
LHIHSRQEEEQSEIMEYSVLLPRTLFQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
KVLGIVVQNTKVANLTEPVVLTFQHQLQPKNVTLQCVFWVEDPTLSSPGHWSSAGCETVRRE
TQTSCFCNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGCVVSALACLVTIAAYLCSRVPLPC
RRKPRDYTIKVHMNLLLAVFLLDTSFLLSEPVALTGSEAGCRASAIFLHFSLLTCLSWMGLE
GYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIY
PSMCWIRDSLVSYITNLGLFSLVFLFNMAMLATMVVQILRLRPHTQKWSHVLTLLGLSLVLG
LPWALIFFSFASGTFQLVVLYLFSIITSFQGFLIFIWYWSMRLQARGGPSPLKSNSDSARLP
ISSGSTSSSRI

Important features:

Signal peptide:

amino acids 1-25

Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590 and 634-657

Microbodies C-terminal targeting signal.

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327 and 341-344

G-protein coupled receptors family 2 proteins

amino acids 475-504

FIGURE 205

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA
GGAAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGG
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG
TGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCT
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT
GGTGTTTCTGTTCAACATGG

FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTCAGGTCCA
GGTTTTGCTTTGATCCTTTTCAAAAACTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTT
GGATGGGATTATGTGGAAACTACCCTGCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCC
ACCCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAAGAGACTCGGGAGTCGCTGCTTCCAAAGT
GCCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAA<u>ATG</u>AGCCTCTTCGGGCTTCTCCTGCT
GACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAAT
TCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATT
ACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAAGAAATAC
GGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTACGTTTGATG
AAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTGTAGAAGTTGAG
GAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAGGAAAACA
GATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCCTTCTGAAC
CAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAGAAGCTGTGAGTCCTTCA
GTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTAC
CTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGCAGTTGGACTTAGAAGATCTAT
ATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTTTTGGAAGAAAATCCAGAGTGGTG
GATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGT
GTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTA
AACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCA
AGCAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGG
ATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCA
GAGGGAGCACAGGAGGA<u>TAG</u>CCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGC
AGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTT
CAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATT
AGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATC
GTGGAAAGAAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTA
CGTATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGT
ACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCC
ATGTCCTGGGCCTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTGCTCATATTCAC
ATATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCT
ATGAATTAAACTTGTGTCATGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAAAAT
TTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAG
AGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTTAT
ATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCTATTTTTAC
CAAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAATT
TTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGAC
AAAAATACATGTATTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAA
CTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTTTTTGAAAATAATTAAATTATCATATC
TTCCATTCCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGAAAGTAGACATTCAGATCC
AGCCATTACTAACCTATTCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGC
ACCTTGAAAAAGACTTGGCAGCTTCCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACAT
CCTATTTATTGTGATGTTGTGGTTTTATTATCTTAAACTCTGTTCCATACACTTGTATAAAT
ACATGGATATTTTTATGTACAGAAGTATGTCTCTTAACCAGTTCACTTATTGTACTCTGGCA
ATTTAAAAGAAAATCAGTAAAATATTTTGCTTGTAAAATGCTTAATATNGTGCCTAGGTTAT
GTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAAATAAAAGAATGTGGCTATTTTGG
GGAGAAAATTAAAAAAAAAAAAAAAAAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

FIGURE 207

MSLFGLLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR
FPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLL
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLY
SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQ
LRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG

FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATT
CCATTTTGGAAGAAGACTAAAAATGGTGTTTCCAATGTGGACACTGAAGAGACAAATTCTTA
TCCTTTTTAACATAATCCTAATTTCCAAACTCCTTGGGGCTAGATGGTTTCCTAAAACTCTG
CCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTGATCGTGGACTGCACAGACAAGCA
TTTGACAGAAATTCCTGGAGGTATTCCCACGAACACCACGAACCTCACCCTCACCATTAACC
ACATACCAGACATCTCCCCAGCGTCCTTTCACAGACTGGACCATCTGGTAGAGATCGATTTC
AGATGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCA
GATTAAACCCAGAAGCTTTAGTGGACTCACTTATTTAAAATCCCTTTACCTGGATGGAAACC
AGCTACTAGAGATACCGCAGGGCCTCCCGCCTAGCTTACAGCTTCTCAGCCTTGAGGCCAAC
AACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCCAACATAGAAATACTCTACCT
GGGCCAAAACTGTTATTATCGAAATCCTTGTTATGTTTCATATTCAATAGAGAAAGATGCCT
TCCTAAACTTGACAAAGTTAAAAGTGCTCTCCCTGAAAGATAACAATGTCACAGCCGTCCCT
ACTGTTTTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCA
AGAAGATGATTTTAATAACCTCAACCAATTACAAATTCTTGACCTAAGTGGAAATTGCCCTC
GTTGTTATAATGCCCCATTTCCTTGTGCGCCGTGTAAAAATAATTCTCCCCTACAGATCCCT
GTAAATGCTTTTGATGCGCTGACAGAATTAAAAGTTTTACGTCTACACAGTAACTCTCTTCA
GCATGTGCCCCCAAGATGGTTTAAGAACATCAACAAACTCCAGGAACTGGATCTGTCCCAAA
ACTTCTTGGCCAAAGAAATTGGGGATGCTAAATTTCTGCATTTCTCCCCAGCCTCATCCAA
TTGGATCTGTCTTTCAATTTTGAACTTCAGGTCTATCGTGCATCTATGAATCTATCACAAGC
ATTTTCTTCACTGAAAAGCCTGAAAATTCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGA
AAAGCTTTAACCTCTCGCCATTACATAATCTTCAAAATCTTGAAGTTCTTGATCTTGGCACT
AACTTTATAAAAATTGCTAACCTCAGCATGTTTAAACAATTTAAAAGACTGAAAGTCATAGA
TCTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAATG
CCAGAACTTCTGTAGAAAGTTATGAACCCCAGGTCCTGGAACAATTACATTATTTCAGATAT
GATAAGTATGCAAGGAGTTGCAGATTCAAAAACAAAGAGGCTTCTTTCATGTCTGTTAATGA
AAGCTGCTACAAGTATGGGCAGACCTTGGATCTAAGTAAAAATAGTATATTTTTTGTCAAGT
CCTCTGATTTTCAGCATCTTTCTTTCCTCAAATGCCTGAATCTGTCAGGAAATCTCATTAGC
CAAACTCTTAATGGCAGTGAATTCCAACCTTTAGCAGAGCTGAGATATTTGGACTTCTCCAA
CAACCGGCTTGATTTACTCCATTCAACAGCATTTGAAGAGCTTCACAAACTGGAAGTTCTGG
ATATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAAACTTTACC
AAGAACCTAAAGGTTCTGCAGAAACTGATGATGAACGACAATGACATCTCTTCCTCCACCAG
CAGGACCATGGAGAGTGAGTCTCTTAGAACTCTGGAATTCAGAGGAAATCACTTAGATGTTT
TATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAGAATCTGCTAAAATTAGAGGAA
TTAGACATCTCTAAAAATTCCCTAAGTTTCTTGCCTTCTGGAGTTTTTGATGGTATGCCTCC
AAATCTAAAGAATCTCTCTTTGGCCAAAAATGGGCTCAAATCTTTCAGTTGGAAGAAACTCC
AGTGTCTAAAGAACCTGGAAACTTTGGACCTCAGCCACAACCAACTGACCACTGTCCCTGAG
AGATTATCCAACTGTTCCAGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAG
TCTGACGAAGTATTTTCTACAAGATGCCTTCCAGTTGCGATATCTGGATCTCAGCTCAAATA
AAATCCAGATGATCCAAAAGACCAGCTTCCCAGAAAATGTCCTCAACAATCTGAAGATGTTG
CTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGGGTTAA
CCATACGGAGGTGACTATTCCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCAC
ACAAGGGCCAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTG
ATTCTGTTCTCACTTTCCATATCTGTATCTCTCTTTCTCATGGTGATGATGACAGCAAGTCA
CCTCTATTTCTGGGATGTGTGGTATATTTACCATTTCTGTAAGGCCAAGATAAAGGGGTATC
AGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTATGACACTAAAGACCCA
GCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAAACTGGAAGACCCAAGAGAGAAACA
TTTTAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAAAACCTTT
CCCAGAGCATACAGCTTAGCAAAAAGACAGTGTTTGTGATGACAGACAAGTATGCAAAGACT
GAAAATTTTAAGATAGCATTTTACTTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGT
GATTATCTTGATATTTCTTGAGAAGCCCTTTCAGAAGTCCAAGTTCCTCCAGCTCCGGAAAA
GGCTCTGTGGGAGTTCTGTCCTTGAGTGGCCAACAAACCCGCAAGCTCACCCATACTTCTGG
CAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGA
AACGGTCTAGCCCTTCTTTGCAAAACACAACTGCCTAGTTTACCAAGGAGAGGCCTGGC

FIGURE 209

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG
IPTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRCNCVPIPLGSKNNMCIKRLQIKPRSFS
GLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGQNCYYR
NPCYVSYSIEKDAFLNLTKLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNL
NQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWF
KNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSL
KILRIRGYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQ
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVLQKLMMNDNDISSSTSRTMESES
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSL
AKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQ
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDAVWFVWWVNHTEVTIP
YLATDVTCVGPGAHKGQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDVW
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPAVTEWVLAELVAKLEDPREKHFNLCLEE
RDWLPGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVIILIFLE
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHPYFWQCLKNALATDNHVAYSQVFKETV

FIGURE 210A

GGGTACCATTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACAACAGAAACATGGAA
AACATGTTCCTTCAGTCGTCAATGCTGACCTGCATTTTCCTGCTAATATCTGGTTCCTGTGA
GTTATGCGCCGAAGAAAATTTTTCTAGAAGCTATCCTTGTGATGAGAAAAAGCAAAATGACT
CAGTTATTGCAGAGTGCAGCAATCGTCGACTACAGGAAGTTCCCCAAACGGTGGCAAATAT
GTGACAGAACTAGACCTGTCTGATAATTTCATCACACACATAACGAATGAATCATTTCAAGG
GCTGCAAAATCTCACTAAAATAAATCTAAACCACAACCCCAATGTACAGCACCAGAACGGAA
ATCCCGGTATACAATCAAATGGCTTGAATATCACAGACGGGGCATTCCTCAACCTAAAAAAC
CTAAGGGAGTTACTGCTTGAAGACAACCAGTTACCCCAAATACCCTCTGGTTTGCCAGAGTC
TTTGACAGAACTTAGTCTAATTCAAAACAATATATACAACATAACTAAAGAGGGCATTTCAA
GACTTATAAACTTGAAAAATCTCTATTTGGCCTGGAACTGCTATTTTAACAAAGTTTGCGAG
AAAACTAACATAGAAGATGGAGTATTTGAAACGCTGACAAATTTGGAGTTGCTATCACTATC
TTTCAATTCTCTTTCACACGTGCCACCCAAACTGCCAAGCTCCCTACGCAAACTTTTTCTGA
GCAACACCCAGATCAAATACATTAGTGAAGAAGATTTCAAGGGATTGATAAATTTAACATTA
CTAGATTTAAGCGGGAACTGTCCGAGGTGCTTCAATGCCCCATTTCCATGCGTGCCTTGTGA
TGGTGGTGCTTCAATTAATATAGATCGTTTTGCTTTTCAAAACTTGACCCAACTTCGATACC
TAAACCTCTCTAGCACTTCCCTCAGGAAGATTAATGCTGCCTGGTTTAAAAATATGCCTCAT
CTGAAGGTGCTGGATCTTGAATTCAACTATTTAGTGGGAGAAATAGTCTCTGGGGCATTTTT
AACGATGCTGCCCCGCTTAGAAATACTTGACTTGTCTTTTAACTATATAAAGGGGAGTTATC
CACAGCATATTAATATTTCCAGAAACTTCTCTAAACTTTTGTCTCTACGGGCATTGCATTTA
AGAGGTTATGTGTTCCAGGAACTCAGAGAAGATGATTTCCAGCCCCTGATGCAGCTTCCAAA
CTTATCGACTATCAACTTGGGTATTAATTTTATTAAGCAAATCGATTTCAAACTTTTCCAAA
ATTTCTCCAATCTGGAAATTATTTACTTGTCAGAAAACAGAATATCACCGTTGGTAAAAGAT
ACCCGGCAGAGTTATGCAAATAGTTCCTCTTTTCAACGTCATATCCGGAAACGACGCTCAAC
AGATTTTGAGTTTGACCCACATTCGAACTTTTATCATTTCACCCGTCCTTTAATAAAGCCAC
AATGTGCTGCTTATGGAAAAGCCTTAGATTTAAGCCTCAACAGTATTTTCTTCATTGGGCCA
AACCAATTTGAAAATCTTCCTGACATTGCCTGTTTAAATCTGTCTGCAAATAGCAATGCTCA
AGTGTTAAGTGGAACTGAATTTTCAGCCATTCCTCATGTCAAATATTTGGATTTGACAAACA
ATAGACTAGACTTTGATAATGCTAGTGCTCTTACTGAATTGTCCGACTTGGAAGTTCTAGAT
CTCAGCTATAATTCACACTATTTCAGAATAGCAGGCGTAACACATCATCTAGAATTTATTCA
AAATTTCACAAATCTAAAAGTTTTAAACTTGAGCCACAACAACATTTATACTTTAACAGATA
AGTATAACCTGGAAAGCAAGTCCCTGGTAGAATTAGTTTTCAGTGGCAATCGCCTTGACATT
TTGTGGAATGATGATGACAACAGGTATATCTCCATTTTCAAAGGTCTCAAGAATCTGACACG
TCTGGATTTATCCCTTAATAGGCTGAAGCACATCCCAAATGAAGCATTCCTTAATTTGCCAG
CGAGTCTCACTGAACTACATATAAATGATAATATGTTAAAGTTTTTTAACTGGACATTACTC
CAGCAGTTTCCTCGTCTCGAGTTGCTTGACTTACGTGGAAACAAACTACTCTTTTTAACTGA
TAGCCTATCTGACTTTACATCTTCCCTTCGGACACTGCTGCTGAGTCATAACAGGATTTCCC
ACCTACCCTCTGGCTTTCTTTCTGAAGTCAGTAGTCTGAAGCACCTCGATTTAAGTTCCAAT
CTGCTAAAAACAATCAACAAATCCGCACTTGAAACTAAGACCACCACCAAATTATCTATGTT
GGAACTACACGGAAACCCCTTTGAATGCACCTGTGACATTGGAGATTTCCGAAGATGGATGG
ATGAACATCTGAATGTCAAAATTCCCAGACTGGTAGATGTCATTTGTGCCAGTCCTGGGGAT
CAAAGAGGGAAGAGTATTGTGAGTCTGGAGCTAACAACTTGTGTTTCAGATGTCACTGCAGT
GATATTATTTTTCTTCACGTTCTTTATCACCACCATGGTTATGTTGGCTGCCCTGGCTCACC
ATTTGTTTTACTGGGATGTTTGGTTTATATATAATGTGTGTTTAGCTAAGGTAAAAGGCTAC
AGGTCTCTTTCCACATCCCAAACTTTCTATGATGCTTACATTTCTTATGACACCAAAGATGC
CTCTGTTACTGACTGGGTGATAAATGAGCTGCGCTACCACCTTGAAGAGAGCCGAGACAAAA
ACGTTCTCCTTTGTCTAGAGGAGAGGGATTGGGACCCGGGATTGGCCATCATCGACAACCTC
ATGCAGAGCATCAACCAAAGCAAGAAAACAGTATTTGTTTTAACCAAAAAATATGCAAAAAG
CTGGAACTTTAAAACAGCTTTTTACTTGGCTTTGCAGAGGCTAATGGATGAGAACATGGATG
TGATTATATTTATCCTGCTGGAGCCAGTGTTACAGCATTCTCAGTATTTGAGGCTACGGCAG
CGGATCTGTAAGAGCTCCATCCTCCAGTGGCCTGACAACCCGAAGGCAGAAGGCTTGTTTTG
GCAAACTCTGAGAAATGTGGTCTTGACTGAAAATGATTCACGGTATAACAATATGTATGTCG
ATTCCATTAAGCAATACTAACTGACGTTAAGTCATGATTTCGCGCCATAATAAAGATGCAAA
GGAATGACATTTCTGTATTAGTTATCTATTGCTATGTAACAAATTATCCCAAAACTTAGTGG
TTTAAAACAACACATTTGCTGGCCCACAGTTTTTGAGGGTCAGGAGTCCAGGCCCAGCATAA

FIGURE 210B

CTGGGTCCTCTGCTCAGGGTGTCTCAGAGGCTGCAATGTAGGTGTTCACCAGAGACATAGGC
ATCACTGGGGTCACACTCATGTGGTTGTTTCTGGATTCAATTCCTCCTGGGCTATTGGCCA
AAGGCTATACTCATGTAAGCCATGCGAGCCTCTCCCACAAGGCAGCTTGCTTCATCAGAGCT
AGCAAAAAAGAGAGGTTGCTAGCAAGATGAAGTCACAATCTTTTGTAATCGAATCAAAAAAG
TGATATCTCATCACTTTGGCCATATTCTATTTGTTAGAAGTAAACCACAGGTCCCACCAGCT
CCATGGGAGTGACCACCTCAGTCCAGGGAAAACAGCTGAAGACCAAGATGGTGAGCTCTGAT
TGCTTCAGTTGGTCATCAACTATTTTCCCTTGACTGCTGTCCTGGGATGGCCTGCTATCTTG
ATGATAGATTGTGAATATCAGGAGGCAGGGATCACTGTGGACCATCTTAGCAGTTGACCTAA
CACATCTTCTTTTCAATATCTAAGAACTTTTGCCACTGTGACTAATGGTCCTAATATTAAGC
TGTTGTTTATATTTATCATATATCTATGGCTACATGGTTATATTATGCTGTGGTTGCGTTCG
GTTTTATTTACAGTTGCTTTTACAAATATTTGCTGTAACATTTGACTTCTAAGGTTTAGATG
CCATTTAAGAACTGAGATGGATAGCTTTTAAAGCATCTTTTACTTCTTACCATTTTTTAAAA
GTATGCAGCTAAATTCGAAGCTTTTGGTCTATATTGTTAATTGCCATTGCTGTAAATCTTAA
AATGAATGAATAAAAATGTTTCATTTTACAAAAAAAAAAAAAAAAA

FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQNDSVIAECSNRRLQEVPQTVG
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHQNGNPGIQSNGLNITDGAFLNL
KNLRELLLEDNQLPQIPSGLPESLTELSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEEDFKGLINL
TLLDLSGNCPRCFNAPFPCVPCDGGASINIDRFAFQNLTQLRYLNLSSTSLRKINAAWFKNM
PHLKVLDLEFNYLVGEIVSGAFLTMLPRLEILDLSFNYIKGSYPQHINISRNFSKLLSLRAL
HLRGYVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNFSNLEIIYLSENRISPLV
KDTRQSYANSSSFQRHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDLEV
LDLSYNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL
DILWNDDDNRYISIFKGLKNLTRLDLSLNRLKHIPNEAFLNLPASLTELHINDNMLKFFNWT
LLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRTLLLSHNRISHLPSGFLSEVSSLKHLDLS
SNLLKTINKSALETKTTTKLSMLELHGNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP
GDQRGKSIVSLELTTCVSDVTAVILFFFTFFITTMVMLAALAHHLFYWDVWFIYNVCLAKVK
GYRSLSTSQTFYDAYISYDTKDASVTDWVINELRYHLEESRDKNVLLCLEERDWDPGLAIID
NLMQSINQSKKTVFVLTKKYAKSWNFKTAFYLALQRLMDENMDVIIFILLEPVLQHSQYLRL
RQRICKSSILQWPDNPKAEGLFWQTLRNVVLTENDSRYNNMYVDSIKQY

FIGURE 212

CCAGGTCCAACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA
GCAGCTCCTGCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA
GGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT
CTGGTGTTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGT
CCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCGTGCAGCGTGTGTACCAGCCCTTCCTCA
CCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC
CGCAGCCCTGGGCTGGCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGAC
CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGA
GCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA
GATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGCCGG
CAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC
CCAAGGGAGGGCCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAA
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGC
CCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC
TGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCCTTCCTG
GAGGAGCAGCTGGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTG
GACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGGTCCAG
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCC
TTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC
CCCTGGCTACCCCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAG
GCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAACGTGA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGT
CGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAAT

FIGURE 213

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

FIGURE 214

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC
AGCAGCATCAGAGCAGCCCCTGTGGTTGGCAGCAAAGTTCAGCTTGGCTGGGCCGCTGTGA
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC
AGTGGATGAGCAACCCAACGGGGGCCCGGGGAGGGGAACTGGCCCCGAGGGAGAGGAACCCC
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCCTGTCCGGGGGATGACTGATTC
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCC<u>ATG</u>AGGGGC
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTTGGCAGTGGGCGGCACAGAGCACGCCTA
CCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCG
TGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC
CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCTGCCAGGCCTCGCTA
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTG
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCC
TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCCAGGGTGGCCCCCAACCCG
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT
GGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGAC
TCCCTGAGCGAGCAGATTTCCTTCCTGGAGGAGCAGCTGGGGTCCTGCTCCTGCAAGAAAGA
CTCG<u>TGA</u>CTGCCCAGCGCTCCAGGCTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATG
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC
AGGGCCTTCCTCCTCTTCCTCCTCCCCTTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCA
TCCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC
CCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC
CCCCAGCACAATAAAAATGAAACGTG

FIGURE 215

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC
CTGGAGGCACAGGCC<u>ATG</u>AGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTTGGC
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACG
GGGACCCTGTCTCCGAGTCGTTCGTGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGAC
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG
GCTGGCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA
ATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT
GCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG
CCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACA
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCC
TTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCCTTCCTGGAGGAGCAGCT
GGGGTCCTGCTCCTGCAAGAAAGACTCG<u>TGA</u>CTGCCCAGCGCCCCAGGCTGGACTGAGCCCC
TCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCCTTCCTCGGGAG
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC
CCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC
GAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGG
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAACGTG

FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTCQSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

FIGURE 218

GGTTGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCTTGTCAGGAGGAGACAGCCTC
CCGGCCCGGGGAGGACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTC
CGTTTCCTGCCGTCAGCTGCCGGCCGAGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTC
CTGGTCTCCCTTCTCCCGCTGGGCCGGTTTATCGGGAGGAGATTGTCTTCCAGGGCTAGCAA
TTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGATTTCAAAGCTG
GGCTCAGCCTCTGTTTCTTCTCTCGTGTAATCGCAAAACCCATTTTGGAGCAGGAATTCCAA
TCATGTCTGTGATGGTGGTGAGAAAGAAGGTGACACGGAAATGGGAGAAACTCCCAGGCAGG
AACACCTTTTGCTGTGATGGCCGCGTCATGATGGCCCGGCAAAAGGGCATTTTCTACCTGAC
CCTTTTCCTCATCCTGGGGACATGTACACTCTTCTTCGCCTTTGAGTGCCGCTACCTGGCTG
TTCAGCTGTCTCCTGCCATCCCTGTATTTGCTGCCATGCTCTTCCTTTTCTCCATGGCTACA
CTGTTGAGGACCAGCTTCAGTGACCCTGGAGTGATTCCTCGGGCGCTACCAGATGAAGCAGC
TTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACCACCGC
CTCGTATCAAGAATTTCCAGATAAACAACCAGATTGTGAAACTGAAATACTGTTACACATGC
AAGATCTTCCGGCCTCCCCGGGCCTCCCATTGCAGCATCTGTGACAACTGTGTGGAGCGCTT
CGACCATCACTGCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTACCGCTACTTCTACC
TCTTCATCCTTTCTCTCTCCCTCCTCACAATCTATGTCTTCGCCTTCAACATCGTCTATGTG
GCCCTCAAATCTTTGAAAATTGGCTTCTTGGAGACATTGAAAGAAACTCCTGGAACTGTTCT
AGAAGTCCTCATTTGCTTCTTTACACTCTGGTCCGTCGTGGGACTGACTGGATTTCATACTT
TCCTCGTGGCTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAAT
CGCGTCCAGAATCCCTACAGCCATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGTGG
CCCCTTGCCCCCCAGTGTGCTGGATCGAAGGGGTATTTTGCCACTGGAGGAAAGTGGAAGTC
GACCTCCCAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCCCAGCCCCCACAGAA
CACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAGA
GCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACT
TTTGTTTGTGTTTAATTAGGGCTATGAGAGATTTCAGGTGAGAAGTTAAACCTGAGACAGAG
AGCAAGTAAGCTGTCCCTTTTAACTGTTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTG
GCATTTTCTTGCTGCAAGCTTTTTTAAATTTCTGAACTCAAGGCAGTGGCAGAAGATGTCAG
TCACCTCTGATAACTGGAAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCTCCATGGCCTCA
GCCACAGGGTCCCCTTGGACCCCCTCTCTTCCCTCCAGATCCCAGCCCTCCTGCTTGGGGTC
ACTGGTCTCATTCTGGGGCTAAAAGTTTTTGAGACTGGCTCAAATCCTCCCAAGCTGCTGCA
CGTGCTGAGTCCAGAGGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTTCTTGG
GGTCTTCAGGACTGAAGAGGAGGGAGAGTGGGGTCAGAAGATTCTCCTGGCCACCAAGTGCC
AGCATTGCCCACAAATCCTTTTAGGAATGGACAGGTACCTTCCACTTGTTGTANNNNNNNN
NNNNNNNNNNNNNNNNNNNNTTGTTTTTCCTTTTGACTCCTGCTCCCATTAGGAGCAGGAATG
GCAGTAATAAAAGTCTGCACTTTGGTCATTTCTTTTCCTCAGAGGAAGCCCGAGTGCTCACT
TAAACACTATCCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGG
AAACCAAGGCACAGAGAGGCTCTCCTCTCCTCTCCTCTCCCCCGATGTACCCTCAAAAAAAA
AAAAATGCTAACCAGTTCTTCCATTAAGCCTCGGCTGAGTGAGGGAAAGCCCAGCACTGCTG
CCCTCTCGGGTAACTCACCCTAAGGCCTCGGCCCACCTCTGGCTATGGTAACCACACTGGGG
GCTTCCTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCCAGAGCCACTTCACCC
TGGGGGTGGGCTGTGGCCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTCAGGGAAGAAG
ATTTATGTATTATATGTGGCTATATTTCCTAGAGCACCTGTGTTTTCCTCTTTCTAAGCCAG
GGTCCTGTCTGGATGACTTATGCGGTGGGGGAGTGTAAACCGGAACTTTTCATCTATTTGAA
GGCGATTAAACTGTGTCTAATGCA

FIGURE 219

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTLFLILGTCTLFFAFECRYLAV
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHCPWVGNCVGKRNYRYFYL
FILSLSLLTIYVFAFNIVYVALKSLKIGFLETLKETPGTVLEVLICFFTLWSVVGLTGFHTF
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSR
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPPEPPEPPQEAAEAEK

FIGURE 220

AAAACCCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT
CCCACAGAGCNCTTCGACCATCACTGCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTA
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCCNCCTCACAATCTATGTCTTCGCCTTCA
ACATCGT

FIGURE 221

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAGAAGA
AAAAAAATCA<u>ATG</u>AAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTC
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACA
TTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTT<u>TGA</u>TGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA
AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAAA

FIGURE 222

MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL
EIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAV
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF

FIGURE 223

GAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATT
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG
ACCAGAG

FIGURE 224

ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGGCCGCGGCCCGGGAGCGGGCCAGCTG
CCGGGAGCCCTGAATCACCGCCTGGCCCGACTCCACCATGAACGTCGCGCTGCAGGAGCTGG
GAGCTGGCAGCAACGTGGGATTCCAGAAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAG
CTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCTGCACTGCTTCTGGGCTGCCTTGT
GGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCTTACAGAGGCCTGCA
TTCGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCTGTGAGGACTTT
TACCAGTTCTCCTGTGGGGGCTGGATTCGGAGGAACCCCCTGCCCGATGGGCGTTCTCGCTG
GAACACCTTCAACAGCCTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAACA
CCACCTTCAACTCCAGCAGTGAAGCTGAGCAGAAGACACAGCGCTTCTACCTATCTTGCCTA
CAGGTGGAGCGCATTGAGGAGCTGGGAGCCCAGCCACTGAGAGACCTCATTGAGAAGATTGG
TGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACTTTATGGAGGTGTTGAAGGCAGTAG
CAGGGACCTACAGGGCCACCCCATTCTTCACCGTCTACATCAGTGCCGACTCTAAGAGTTCC
AACAGCAATGTTATCCAGGTGGACCAGTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTT
AAACAGAACTGCCAATGAGAAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACTGGGGA
TGCTGCTGGGTGGGCGGCCCACCTCCACGAGGGAGCAGATGCAGCAGGTGCTGGAGTTGGAG
ATACAGCTGGCCAACATCACAGTGCCCCAGGACCAGCGGCGCGACGAGGAGAAGATCTACCA
CAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTCCTGT
CTTTCTTGCTGTCACCATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGAT
TATTTGCAGCAGGTGTCAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCT
GATCTGGAACCTGGTGCAAAAGACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAG
AGAAGCTGCTGGAGACCCTCTATGGCACTAAGAAGTCCTGTGTGCCGAGGTGGCAGACCTGC
ATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTCGTGAAGGCCACGTT
TGACCGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAGG
AGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCA
GATGCCATCTATGATATGATTGGTTTCCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGA
TGTTTATGACGGGTACGAAATTTCTGAAGATTCTTTCTTCCAAAACATGTTGAATTTGTACA
ACTTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAGCCTCCCAGCCGAGACCAGTGGAGC
ATGACCCCCCAGACAGTGAATGCCTACTACCTTCCAACTAAGAATGAGATCGTCTTCCCCGC
TGGCATCCTGCAGGCCCCCTTCTATGCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCA
TCGGTGTGGTCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGAC
AAAGAAGGGAACCTGCGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACAC
GGCCTGCATGGAGGAACAGTACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCC
AGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAA
GCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCA
GCTCTTCTTCGTGGGATTTGCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACG
AGGGGCTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAAC
TCCCGTGACTTCCTGCGGCACTTCGGCTGCCCTGTCGGCTCCCCCATGAACCCAGGGCAGCT
GTGTGAGGTGTGGTAGACCTGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGGCA
GCTCTCCTGACAAAGCTGTTTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGT
CTAGTCCCTCCCCCCCACAGGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCT
CTGCTTTGGGGGTGCCCCTGCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGT
GTCACCCTGCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC

FIGURE 225

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSH
STCLTEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQA
ILKHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDN
FMEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSRDYYLNRTANEKVLTAY
LDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP
SMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL
DRRFESAQEKLLETLYGTKKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI
SEIRTAFEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF
FQNMLNLYNFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLPTKNEIVFPAGILQAPFYARNH
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCS
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNPGQLCEVW

FIGURE 226A

GCCCGGCCCTCCGCCCTCCGCACTCCCGCCTCCCTCCCTCCGCCCGCTCCCGCGCCCTCCTC
CCTCCCTCCTCCCCAGCTGTCCCGTTCGCGTCATGCCGAGCCTCCCGGCCCCGCCGGCCCCG
CTGCTGCTCCTCGGGCTGCTGCTGCTCGGCTCCCGGCCGGCCCGCGGCGCCGGCCCAGAGCC
CCCCGTGCTGCCCATCCGTTCTGAGAAGGAGCCGCTGCCCGTTCGGGGAGCGGCAGGTAGGT
GGGCGCCCGGGGGAGGCGCGGGCGGGGAGTCGGGCTCGGGGCGAGTCAGCGCCAGCCCGGAG
GGGGCGCGGGGCGCAGGTGGCTCGGCGCGGCGGGCGGCCCGGAGGGTGGGCGGGGGCAGAAG
GGCGCGGTGCCTGGGACCCGGGACCCGCGGGCAGCCCCCGGGGCGGCACACGGCGCGAGCTG
GGCAGCGGCCTCCAGCCAAGCCCGTCCCCGCAGGCTGCACCTTCGGCGGGAAGGTCTATGCC
TTGGACGAGACGTGGCACCCGGACCTAGGGGAGCCATTCGGGGTGATGCGCTGCGTGCTGTG
CGCCTGCGAGGCGCAGTGGGGTCGCCGTACCAGGGGCCCTGGCAGGGTCAGCTGCAAGAACA
TCAAACCAGAGTGCCCAACCCCGGCCTGTGGGCAGCCGCGCCAGCTGCCGGGACACTGCTGC
CAGACCTGCCCCCAGGACTTCGTGGCGCTGCTGACAGGGCCGAGGTCGCAGGCGGTGGCACG
AGCCCGAGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCCTACAGGCGGCTGGACC
GCCCTACCAGGATCCGCTTCTCAGACTCCAATGGCAGTGTCCTGTTTGAGCACCCTGCAGCC
CCCACCCAAGATGGCCTGGTCTGTGGGGTGTGGCGGGCAGTGCCTCGGTTGTCTCTGCGGCT
CCTTAGGGCAGAACAGCTGCATGTGGCACTTGTGACACTCACTCACCCTTCAGGGGAGGTCT
GGGGGCCTCTCATCCGGCACCGGGCCCTGTCCCCAGAGACCTTCAGTGCCATCCTGACTCTA
GAAGGCCCCCACCAGCAGGGCGTAGGGGGCATCACCCTGCTCACTCTCAGTGACACAGAGGA
CTCCTTGCATTTTTTGCTGCTCTTCCGAGGCCTTGCAGGACTAACCCAGGTTCCCTTGAGGC
TCCAGATTCTACACCAGGGGCAGCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCAGGAA
CCAGGCTTTGCTGAGGTGCTGCCCAACCTGACAGTCCAGGAGATGGACTGGCTGGTGCTGGG
GGAGCTGCAGATGGCCCTGGAGTGGGCAGGCAGGCCAGGGCTGCGCATCAGTGGACACATTG
CTGCCAGGAAGAGCTGCGACGTCCTGCAAAGTGTCCTTTGTGGGGCTAATGCCCTGATCCCA
GTCCAAACGGGTGCTGCCGGCTCAGCCAGCCTCACTCTGCTAGGAAATGGCNCCCTGATCCT
CCAGGTGCAATTGGTAGGGACAACCAGTGAGGTGGTGGCCATGACACTGGAAACCAAGCCTC
AGCGGAGGGATCAGCCCACTGTCCTGTGCCACATGGCTGGCCTATCCTCCCCTGCCCCCAGG
CCGTGGGTATCTGCCCTGGGCTGGGGTGCCCGAGGGGCTCATATGCTGCTGCAGAATGAGCT
CTTCCTGAACGTGGGCACCAAGGACTTCCCAGACGGAGAGCTTCGGGGGCAACGTGGCTGCC
CTGCCCTACTGTGGGGCATAGCGCCCGCCCTGCCCGTGCCCCTAGCAGGAGCCCTGGTGCTA
CCCCCTGTGAAGAGCCAAGCAGCAGGGCACGCCTGGCTTTCCTTGGATACCCACTGTCACCT
GCACTATGAAGTGCTGCTGGCTGGGCTTGGTGGCTCAGAACAAGGCACTGTCACTGCCCACC
TCCTTGGGCCTCCTGGAACGCCAGGGCCTCGGCGGCTGCTGAAGGGATTCTATGGCTCAGAG
GCCCAGGGTGTGGTGAAGGACCTGGAGCCGGAACTGCTGCGGCACCTGGCAAAAGGCATGGC
TTCCCTGATGATCACCACCAAGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGCCTCTCCTCCC
AGGTGCACATAGCCAACCAATGTGAGGTTGGCGGACTGCGCCTGGAGGCGGCCGGGGCCGAG
GGGGTGCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCCTGTGGTGCCTGGTCT
CCCGGCCCTAGCGCCCGCCAAACCTGGTGGTCCTGGGCGGCCCCGAGACCCCAACACATGCT
TCTTCGAGGGGCAGCAGCGCCCCCACGGGGCTCGCTGGGCGCCCAACTACGACCCGCTCTGC
TCACTCTGCACCTGCCAGAGACGAACGGTGATCTGTGACCCGGTGGTGTGCCCACCGCCCAG
CTGCCCACACCCGGTGCAGGCTCCCGACCAGTGCTGCCCTGTTTGCCCTGGCTGCTATTTTG
ATGGTGACCGGAGCTGGCGGGCAGCGGGTACGCGGTGGCACCCCGTTGTGCCCCCCTTTGGC
TTAATTAAGTGTGCTGTCTGCACCTGCAAGCAGGGGGGCACTGGAGAGGTGCACTGTGAGAA
GGTGCAGTGTCCCCGGCTGGCCTGTGCCCAGCCTGTGCGTGTCAACCCCACCGACTGCTGCA
AACAGTGTCCAGGTGAGGCCCACCCCCAGCTGGGGGACCCCATGCAGGCTGATGGGCCCCGG
GGCTGCCGTTTTGCTGGGCAGTGGTTCCCAGAGAGTCAGAGCTGGCACCCCTCAGTGCCCCC
GTTTGGAGAGATGAGCTGTATCACCTGCAGATGTGGGGTAAGTGGGGAGCAGAGGCTTGTGT
GAGGTGGGTACTGGGAGCCTGGTCTGGAGTAGGGAGACCTTCCCAGGGAGGTCCCTGAAGAA
GCTGAAGGTCACTGTGTCCCAGTGCCTCTGGGGGACACTCAGTGTCTGCTCTGTCTTGTACC
AGGCAGGGGTGCCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGTCCTGTGGCTCGGGG
AAGGAGAGTCGATGCTGTTCCCGCTGCACGGCCCACCGGCGGCGTAAGTGAGGGAGTCCAGG
GTCAGCAGCTGTGAGTGGAGGGCTCACCTGCCTGTGGGACTCCTGATCAGGGAAGGGAGCAC
TCACTGTGTGCAGGAACAGTGCAGCCTGCCTCACAAGTGCCATTCCAATCCACCCTCACAGC
AACCTGGTGGAATTGTTATTTATGACCTTTTCTTTACAAATGAGATTTCTGAAGCTCAGAGA
AATTAAGCAACGAGATGAAGGTCACCCAGCTGTGTGCACTGACCTGTTTAGAAAATACTGGC

FIGURE 226B

CTTTCTGGGACCAAGGCAGGGATGCTTTGCCCTGCCCTCTATGCCTCTCTGTGCCTCTCCAC
TCCCTCTCCCCTCCTCCAACATTCCCTCCCTTCTGTCTCCAGCAGCCCCAGAGACCAGAACT
GATCCAGAGCTGGAGAAAGAAGCCGAAGGCTCTTAGGGAGCAGCCAGAGGGCCAAGTGACCA
AGAGGATGGGGCCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTTGCATTCTCCTGTGG
GAAGCCCAGTGCCTTTGCTCCTCTGTCCTGCCTCTACTCCCACCCCCACTACCTCTGGGAAC
CACAGCTCCACAAGGGGGAGAGGCAGCTGGGCCAGACCGAGGTCACAGCCACTCCAAGTCCT
GCCCTGCCACCCTCGGCCTCTGTCCTGGAAGCCCCACCCCTTTCTTCCTGTACATAATGTCA
CTGGCTTGTTGGGATTTTTAATTTATCTTCACTCAGCACCAAGGGCCCCGGACACTCCACTC
CTGCTGCCCCTGAGCTGAGCAGAGTCATTATTGGAGAGTTTTGTATTTATTAAAACATTTCT
TTTTCAGTCTTTGGGCATGAGGTTGGCTCTTTGTGGCCAGGAACCTGAGTGGGGCCTGGTGG
AGAAGGGGCNGAGAGTAGGAGGTGAGAGAGAGGAGCTCTGACACTTGGGGAGCTGAAAGAGA
CCTGGAGAGGCAGAGGATAGCGTGGCNNTTGGCTGGCATNCCTGGGTTCCGCAGAGGGGCTG
GGGATGGTTCTTGAGATGGTCTAGAGACTCAAGAATTTAGGGAAGTAGAAGCAGGATTTTGA
CTCAAGTTTAGTTTCCCACATCGCTGGCCTGTTTGCTGACTTCATGTTTGAAGTTGCTCCAG
AGAGAGAATCAAAGGTGTCACCAGCCCCTCTCTCCCTCCTTCCCTTCCCTTCCCTTTCTTTC
CCTCCCCTCCCCTCCCCTCCCCTCCCCTCC

FIGURE 227

GGCCGAGCGGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA
CCGGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCGAC
TCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTCGAGTGGCTGGAAAAATCCTGGAGTCCCT
GGACCGAGGGGTGAGCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTCGGA
GGAACCCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTCTTCAC
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTCACCTAGTGAACAAACTGCCCCT
CCTTTCTTTCTTCTTTTCTTCCTCCCTCCCTCCCTTTCTTCCCCTTTTCCTTCCTTCCTTCC
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTCG
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTCGATGGGTTCATGGACCT
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCCTGAGGATTCAGGAGAGACTTATGGAGCC
AGCAAAGTCTTCCTGAAGAGATTGCATTTGAGCCAGGTCCTGTAG

FIGURE 228

ATGCCTACTACCTTCCAACTAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC
TTCTATGCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAG
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGCTGGTGACCGACCC
CCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACTCCCGTGACTTCCTGCGGC
ACTTCGGCTGCCCTGTCGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC
TGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGGCAGCTCTCCTGACAAAGCTGT
TTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACA
GGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCCT
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGTGTCACCCTGCCTGGAAGAG
GTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCCTCTTCTGTCCCCAGGCTCACT
CAGCCTGGCGGCCATGGGGCCTGCCGTGCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCGCACTTAGGGGTGGACTCAGCTCTGTC
TGGCTCACCCTCACGGGCTACCCCCACCTCACCCTGTGCTCCTTGTGCCACTGCTCCCAGTG
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCATATGTGTAGCGGGTACTGGTTCCTGT
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT
TGGCCCTTATAGGACC